

Result No.	Score	Query Match	Length	DB ID	Description
1	344	100.0	344	21	AA818994
2	344	100.0	344	21	AA818904
3	344	100.0	344	21	AAB08825
4	344	100.0	344	21	AA808317
5	344	100.0	344	21	AA808341
6	344	100.0	344	21	AA93341
7	344	100.0	344	22	AA663698
8	344	100.0	344	22	AA567770
9	344	100.0	344	23	AA848395
10	344	100.0	344	23	AA447796

84	9	2.6	1061	21	AA80568	Wild type Escheric	157	8	2.3	537	20	AA03839	Chimeric transcrip
85	9	2.6	2639	22	ABG15016	Novel human diagno	158	8	2.3	550	14	AA42085	NF-kappaB p65.pro
86	8	2.3	10	23	AB78543	Glycomodule relate	159	8	2.3	550	14	AA42254	Human p65 protein
87	8	2.3	15	12	AA12480	"Hydrophobic tail"	160	8	2.3	550	14	AA42255	Human p65 protein
88	8	2.3	26	20	AA03840	Alanine/proline ri	161	8	2.3	551	21	AA94383	Human NF-kappa-B p
89	8	2.3	41	20	AA49097	Amino acid sequenc	162	8	2.3	581	22	AB55842	Drosophila melanog
90	8	2.3	43	20	AA49096	Amino acid sequenc	163	8	2.3	581	22	AB55842	Drosophila melanog
91	8	2.3	51	22	AAU62252	Protonibacterium	164	8	2.3	609	19	AAW83215	Human h-NUMB-R. H
92	8	2.3	52	23	ABP08909	Human OREF protein	165	8	2.3	627	20	AA01495	Rat pan-s/tk recep
93	8	2.3	60	22	AB338355	Peptide #581 enco	166	8	2.3	630	23	AB80765	Geneswitch regulat
94	8	2.3	60	22	AB23532	Protein #5531 enco	167	8	2.3	630	23	AB80766	Truncated GAL4 DBD
95	8	2.3	60	22	AAW58966	Human brain expres	168	8	2.3	645	22	AAU2531	Human mdm1 protein
96	8	2.3	60	22	AAW71493	Human bone marrow	169	8	2.3	645	22	AAU2531	Human mdm1 protein
97	8	2.3	60	22	AAW19146	Peptide #580 enco	170	8	2.3	654	23	AB80764	Candida albicans p
98	8	2.3	60	22	AAW19146	Peptide #581 enco	171	8	2.3	654	23	AB80764	Candida albicans p
99	8	2.3	60	23	ABG41306	Human peptide enco	172	8	2.3	701	23	AB80815	Human cytoskeleton
100	8	2.3	77	20	AA41590	Fragment of human	173	8	2.3	701	23	AB80815	Human cytoskeleton
101	8	2.3	86	21	AAW08968	Arabidopsis thalia	174	8	2.3	773	22	ABG15688	Novel human diagno
102	8	2.3	86	21	AAW08968	Arabidopsis thalia	175	8	2.3	773	22	ABG15688	Novel human diagno
103	8	2.3	86	21	AAW08968	Arabidopsis thalia	176	8	2.3	796	22	ABG15688	Novel human diagno
104	8	2.3	86	21	AAW08968	Arabidopsis thalia	177	8	2.3	796	22	ABG15688	Novel human diagno
105	8	2.3	90	22	AB71172	Human nervous syst	178	8	2.3	797	19	AAW85042	PKB-green fluoresc
106	8	2.3	100	14	AAW42120	Oxalacetate decarb	179	8	2.3	797	19	AAW85042	PKB-green fluoresc
107	8	2.3	103	23	AB78540	Ala-Pro-Ala-Pro co	180	8	2.3	797	21	AAW70782	EGFP-NFKappaB fusi
108	8	2.3	120	21	AAW23292	Arabidopsis thalia	181	8	2.3	797	21	AAW70782	EGFP-NFKappaB fusi
109	8	2.3	128	22	AAW0159	Human protein SEQ	182	8	2.3	803	22	AAW79014	Human protein SEQ
110	8	2.3	129	18	AAW14573	Streptococcus pneu	183	8	2.3	803	22	AAW79014	Human protein SEQ
111	8	2.3	131	21	AAW08967	Arabidopsis thalia	184	8	2.3	805	21	AAW22940	GFP-NF-kappa-B fus
112	8	2.3	131	21	AAW46356	Arabidopsis thalia	185	8	2.3	805	21	AAW22940	GFP-NF-kappa-B fus
113	8	2.3	148	20	AAW41588	Fragment of human	186	8	2.3	809	21	AAW84881	Amino acid sequenc
114	8	2.3	167	18	AAW14575	Streptococcus pneu	187	8	2.3	860	21	AAW84881	Amino acid sequenc
115	8	2.3	170	22	ABG1185	Drosophila melanog	188	8	2.3	891	23	AAO22162	Ramoplanin biosynt
116	8	2.3	180	18	AAW14562	Streptococcus pneu	189	8	2.3	904	22	ABW79958	Human protein SEQ
117	8	2.3	183	18	AAW14570	Streptococcus pneu	190	8	2.3	1015	22	ABW79958	Human protein SEQ
118	8	2.3	187	18	AAW14579	Streptococcus pneu	191	8	2.3	1087	22	ABW79958	Human protein SEQ
119	8	2.3	188	18	AAW14580	Streptococcus pneu	192	8	2.3	1088	20	AAW06527	Human cancer-inhib
120	8	2.3	190	18	AAW14569	Streptococcus pneu	193	8	2.3	1088	20	AAW06527	Human cancer-inhib
121	8	2.3	191	22	AAW0126	C glutamic prote	194	8	2.3	1088	20	AAW06527	Human cancer-inhib
122	8	2.3	194	18	AAW14584	Streptococcus pneu	195	8	2.3	1088	20	AAW06527	Human cancer-inhib
123	8	2.3	197	19	AAW0218	Human mcl-1. Homo	196	8	2.3	1088	20	AAW06527	Human cancer-inhib
124	8	2.3	202	22	ABG1097	Drosophila melanog	197	8	2.3	1088	20	AAW06527	Human cancer-inhib
125	8	2.3	204	18	AAW14578	Streptococcus pneu	198	8	2.3	1088	20	AAW06527	Human cancer-inhib
126	8	2.3	206	18	AAW14574	Streptococcus pneu	199	8	2.3	1088	20	AAW06527	Human cancer-inhib
127	8	2.3	233	21	AAW85188	Streptococcus pneu	200	8	2.3	1088	20	AAW06527	Human cancer-inhib
128	8	2.3	251	21	AAW32248	Streptococcus pneu	201	8	2.3	1088	20	AAW06527	Human cancer-inhib
129	8	2.3	251	21	AAW32248	Streptococcus pneu	202	8	2.3	1088	20	AAW06527	Human cancer-inhib
130	8	2.3	254	21	AAW32247	Arabidopsis thalia	203	8	2.3	1088	20	AAW06527	Human cancer-inhib
131	8	2.3	254	21	AAW32247	Arabidopsis thalia	204	8	2.3	1088	20	AAW06527	Human cancer-inhib
132	8	2.3	254	21	AAW32247	Arabidopsis thalia	205	8	2.3	1088	20	AAW06527	Human cancer-inhib
133	8	2.3	280	21	AAW32247	Arabidopsis thalia	206	8	2.3	1088	20	AAW06527	Human cancer-inhib
134	8	2.3	281	21	AAW32246	Arabidopsis thalia	207	8	2.3	1088	20	AAW06527	Human cancer-inhib
135	8	2.3	283	21	AAW32246	Arabidopsis thalia	208	8	2.3	1088	20	AAW06527	Human cancer-inhib
136	8	2.3	283	21	AAW32246	Arabidopsis thalia	209	8	2.3	1088	20	AAW06527	Human cancer-inhib
137	8	2.3	283	21	AAW32246	Arabidopsis thalia	210	8	2.3	1088	20	AAW06527	Human cancer-inhib
138	8	2.3	283	21	AAW32246	Arabidopsis thalia	211	8	2.3	1088	20	AAW06527	Human cancer-inhib
139	8	2.3	313	22	AAU38739	Human polyptide	212	8	2.3	1088	20	AAW06527	Human cancer-inhib
140	8	2.3	317	22	AAW0791	Streptomyces plica	213	8	2.3	1088	20	AAW06527	Human cancer-inhib
141	8	2.3	317	22	AAW0791	Streptomyces plica	214	8	2.3	1088	20	AAW06527	Human cancer-inhib
142	8	2.3	332	22	AAU17475	Human polyptide	215	8	2.3	1088	20	AAW06527	Human cancer-inhib
143	8	2.3	332	22	AAU17475	Human polyptide	216	8	2.3	1088	20	AAW06527	Human cancer-inhib
144	8	2.3	353	22	AAW47447	Novel signal trans	217	8	2.3	1088	20	AAW06527	Human cancer-inhib
145	8	2.3	354	22	ABW69632	MOMP P5. Haemophi	218	8	2.3	1088	20	AAW06527	Human cancer-inhib
146	8	2.3	355	16	AAW42226	Drosophila melanog	219	8	2.3	1088	20	AAW06527	Human cancer-inhib
147	8	2.3	355	16	AAW42226	Drosophila melanog	220	8	2.3	1088	20	AAW06527	Human cancer-inhib
148	8	2.3	358	21	AAW22919	Human FK506-bindin	221	8	2.3	1088	20	AAW06527	Human cancer-inhib
149	8	2.3	375	22	ABW71846	Arabidopsis thalia	222	8	2.3	1088	20	AAW06527	Human cancer-inhib
150	8	2.3	392	22	ABW71846	Arabidopsis thalia	223	8	2.3	1088	20	AAW06527	Human cancer-inhib
151	8	2.3	404	19	AAW68408	Human protein SEQ	224	8	2.3	1088	20	AAW06527	Human cancer-inhib
152	8	2.3	437	22	AAU02965	Drosophila melanog	225	8	2.3	1088	20	AAW06527	Human cancer-inhib
153	8	2.3	497	21	AAW44523	Aujszky's disease	226	8	2.3	1088	20	AAW06527	Human cancer-inhib
154	8	2.3	498	21	AAW44523	Angiotensin conver	227	8	2.3	1088	20	AAW06527	Human cancer-inhib
155	8	2.3	511	22	ABG19456	Mouse diacylglycer	228	8	2.3	1088	20	AAW06527	Human cancer-inhib
156	8	2.3	516	20	AAW55928	Novel human diagno	229	8	2.3	1088	20	AAW06527	Human cancer-inhib
	8	2.3	520	20	AAW01496	Human pan-s/tk-1A		8	2.3	1088	20	AAW06527	Human cancer-inhib
	8	2.3	520	20	AAW01497	Human pan-s/tk-1B		8	2.3	1088	20	AAW06527	Human cancer-inhib

Chimeric transcrip  
NF-kappaB p65.pro  
Human p65 protein  
Human p65 protein  
Human NF-kappa-B p  
Drosophila melanog  
Human h-NUMB-R. H  
Rat pan-s/tk recep  
Geneswitch regulat  
Truncated GAL4 DBD  
Human mdm1 protein  
Candida albicans p  
Geneswitch regulat  
Human cytoskeleton  
Novel human diagno  
Drosophila melanog  
PKB-green fluoresc  
NFKappaB p65 subun  
EGFP-NFKappaB fusi  
NFKappaB-EGFP fusi  
Human protein SEQ  
GFP-NF-kappa-B fus  
Amino acid sequenc  
Balanus amphitrite  
Ramoplanin biosynt  
Human protein SEQ  
Drosophila melanog  
Human cancer-inhib  
Human WART2, ortho  
Amino acid sequenc  
Amino acid sequenc  
Amino acid sequenc  
Drosophila melanog  
Drosophila melanog  
Plasmodium falci  
Protein encoded by  
Hook region #1 con  
Hook region #2 con  
Hook region #10 co  
Hook region #10 co  
Peptide produced b  
N-terminal C76 gly  
Amino acid sequenc  
Human zinc carboxy  
Human zinc carboxy  
Arabidopsis thalia  
Hook region #3 con  
Hook region #9 con  
B.cathartalis CD e  
Protonibacterium  
A leader peptide M  
Modified LE leade  
Protonibacterium  
Human epidermal gr  
Peptide encoded by  
Peptide MSI-1922.  
Human epidermal gr  
Stem cell mobilis  
Human chemokine MI  
Human MIP-3alpha p  
Novel human diagno  
Transforming growt  
Drosophila melanog  
Human secreted pro  
Human 5' EST sece  
HCV II chimeric ep

230	7	2.0	88	23	ABP03258	Human ORFX protein	303	7	2.0	159	20	AAW89682	Osteogenic fusion
231	7	2.0	89	22	AAW67372	Amino acid sequenc	304	7	2.0	172	14	AAW44753	Osteogenic fusion
232	7	2.0	89	23	ABP11383	Human ORFX protein	305	7	2.0	172	15	AAW51659	Osteogenic fusion
233	7	2.0	90	5	AAW40024	Short fusion protei	306	7	2.0	172	17	AAW85769	CBMP2B1 fusion pro
234	7	2.0	95	19	AAW61279	Exodus protein. H	307	7	2.0	172	19	AAW44309	Human osteogenic f
235	7	2.0	95	21	AAW07939	A human C-C chemok	308	7	2.0	172	20	AAW43120	CBMP2B fusion prot
236	7	2.0	96	17	AAW95990	Liver expressed ch	309	7	2.0	172	20	AAW89686	Osteogenic fusion
237	7	2.0	96	17	AAW93086	Human chemokine be	310	7	2.0	177	20	AAW99644	Hepatitis C virus
238	7	2.0	96	18	AAW22669	Human chemokine be	311	7	2.0	177	21	AAW07298	Arabidopsis thalia
239	7	2.0	96	19	AAW57475	Human chemokine be	312	7	2.0	177	21	AAW53696	Arabidopsis thalia
240	7	2.0	96	19	AAW44398	Human liver and ac	313	7	2.0	177	21	AAW80194	Hepatitis C virus
241	7	2.0	96	20	AAW41163	Human chemokine MI	314	7	2.0	178	22	AAW48072	Human extracellular
242	7	2.0	96	21	AAW97074	Human chemokine be	315	7	2.0	180	21	AAW24658	Plant SDF encoded
243	7	2.0	96	21	AAW95535	Human chemokine MI	316	7	2.0	180	21	AAW24658	Plant SDF encoded
244	7	2.0	96	22	AAW31794	Human chemokine be	317	7	2.0	180	21	AAW59347	Growth factor thalia
245	7	2.0	96	23	ABG60667	Small inducible cy	318	7	2.0	182	18	AAW32479	LHL growth factor
246	7	2.0	96	23	AAO19996	Protein of human c	319	7	2.0	182	20	AAW06907	LHL growth factor
247	7	2.0	96	23	AAW15750	Human chemokine be	320	7	2.0	183	21	AAW31245	Arabidopsis thalia
248	7	2.0	96	23	AAW67371	Amino acid sequenc	321	7	2.0	184	18	AAW14589	Streptococcus pneu
249	7	2.0	101	17	AAW95344	HCV I chimeric epi	322	7	2.0	185	18	AAW14566	Streptococcus pneu
250	7	2.0	111	22	ABW39430	Peptide #6936 enco	323	7	2.0	187	21	AAW07573	Protein encoded by
251	7	2.0	111	22	ABW34202	Protein #6201 enco	324	7	2.0	193	9	AAW08877	Hook region #8 con
252	7	2.0	111	22	AAW60110	Human brain expres	325	7	2.0	209	21	AAW50176	Arabidopsis thalia
253	7	2.0	111	22	AAW27222	Human bone marrow	326	7	2.0	212	18	AAW14588	Streptococcus pneu
254	7	2.0	111	22	AAW19703	Peptide #6137 enco	327	7	2.0	212	21	AAW05693	Arabidopsis thalia
255	7	2.0	111	22	AAW32953	Peptide #6990 enco	328	7	2.0	213	18	AAW14567	Streptococcus pneu
256	7	2.0	111	23	ABG42546	Human peptide enco	329	7	2.0	214	22	AAW60079	Human breast cance
257	7	2.0	112	16	AAW74774	Human epidermal gr	330	7	2.0	219	21	AAW33440	Zea mays protein f
258	7	2.0	112	21	AAW42114	Zea mays protein f	331	7	2.0	223	22	ABW67729	Drosophila melanog
259	7	2.0	113	22	AAW50177	Arabidopsis thalia	332	7	2.0	225	8	AAW70359	Sequence encoded b
260	7	2.0	113	22	AAU40453	Propionibacterium	333	7	2.0	225	8	AAW70061	Sequence of human
261	7	2.0	113	22	ABW39444	Peptide #6950 enco	334	7	2.0	227	20	AAW38860	Neisseria meningit
262	7	2.0	113	22	ABW24209	Protein #6208 enco	335	7	2.0	227	20	AAW38862	Neisseria gonorrh
263	7	2.0	113	22	AAW60131	Human brain expres	336	7	2.0	230	22	AAW30210	Sequence of antige
264	7	2.0	113	22	AAW72745	Human bone marrow	337	7	2.0	231	22	ABW64660	Drosophila melanog
265	7	2.0	113	22	AAW32973	Peptide #7010 enco	338	7	2.0	233	4	AAW30204	Sequence encoded b
266	7	2.0	113	23	ABG42569	Human peptide enco	339	7	2.0	233	4	AAW30209	Sequence of antige
267	7	2.0	117	21	AAW42113	Zea mays protein f	340	7	2.0	234	4	AAW30208	Sequence of an FMD
268	7	2.0	121	20	AAW16172	Human novel secret	341	7	2.0	235	4	AAW30211	Sequence of antige
269	7	2.0	122	20	AAW38861	Neisseria gonorrh	342	7	2.0	238	18	AAW14587	Streptococcus pneu
270	7	2.0	128	22	ABW30031	Peptide #2682 enco	343	7	2.0	246	21	AAW10846	Arabidopsis thalia
271	7	2.0	128	22	ABW35203	Peptide #2709 enco	344	7	2.0	246	21	AAW45067	Arabidopsis thalia
272	7	2.0	128	22	ABW20644	Protein #2643 enco	345	7	2.0	248	4	AAW30207	Sequence of an FMD
273	7	2.0	128	22	AAW56035	Human brain expres	346	7	2.0	248	21	AAW10786	Arabidopsis thalia
274	7	2.0	128	22	AAW68405	Human bone marrow	347	7	2.0	249	21	AAW47125	Arabidopsis thalia
275	7	2.0	128	22	AAW16221	Peptide #2655 enco	348	7	2.0	251	21	AAW31244	Arabidopsis thalia
276	7	2.0	128	22	AAW28711	Peptide #2748 enco	349	7	2.0	251	21	AAW45066	Arabidopsis thalia
277	7	2.0	128	22	AAW03951	Peptide #2633 enco	350	7	2.0	251	21	AAW77121	Human neurotransmi
278	7	2.0	128	22	ABW37979	Human peptide enco	351	7	2.0	252	21	AAW10845	Arabidopsis thalia
279	7	2.0	129	22	ABW96320	Human testicular a	352	7	2.0	252	23	AAW31243	Arabidopsis thalia
280	7	2.0	129	22	AAW95789	Human reproductive	353	7	2.0	255	23	AAW83190	Arabidopsis thalia
281	7	2.0	130	22	AAW59193	Propionibacterium	354	7	2.0	255	23	AAW17482	Novel secreted pro
282	7	2.0	131	21	AAW10847	Arabidopsis thalia	355	7	2.0	258	23	AAW52686	Human leucine-rich
283	7	2.0	131	21	AAW26759	Arabidopsis thalia	356	7	2.0	260	21	AAW10785	Human myelin prote
284	7	2.0	131	21	AAW45068	Zea mays protein f	357	7	2.0	260	21	AAW47124	Arabidopsis thalia
285	7	2.0	133	20	AAW25606	Parietaria sp. all	358	7	2.0	262	5	AAW40023	Fusion protein con
286	7	2.0	134	21	AAW02224	Human secreted pro	359	7	2.0	263	22	ABW08077	Novel human diagno
287	7	2.0	138	20	AAW25610	Parietaria sp. all	360	7	2.0	267	22	AAW31012	Novel human secret
288	7	2.0	142	22	ABW11242	Human SLIT-2 homol	361	7	2.0	268	21	AAW07297	Arabidopsis thalia
289	7	2.0	151	22	ABW17851	Human nervous syst	362	7	2.0	268	21	AAW07297	Arabidopsis thalia
290	7	2.0	155	22	AAW35566	Haemophilus influe	363	7	2.0	269	12	AAW11957	Fb-Fb-truncated "
291	7	2.0	158	21	AAW42112	Zea mays protein f	364	7	2.0	270	20	AAW43978	Human protein kina
292	7	2.0	159	22	ABW26467	Novel human diagno	365	7	2.0	270	20	AAW43979	Human protein kina
293	7	2.0	165	22	AAW66561	Human secreted met	366	7	2.0	272	21	AAW43956	Zea mays protein f
294	7	2.0	166	8	AAW70358	Sequence encoded b	367	7	2.0	276	21	AAW43955	Zea mays protein f
295	7	2.0	166	8	AAW70062	Sequence of human	368	7	2.0	277	20	AAW42775	Rat neuronal lmed
296	7	2.0	166	18	AAW14568	Streptococcus pneu	369	7	2.0	279	21	AAW07296	Arabidopsis thalia
297	7	2.0	166	21	AAW26757	Zea mays protein f	370	7	2.0	279	21	AAW53694	Arabidopsis thalia
298	7	2.0	169	14	AAW44749	Osteogenic fusion	371	7	2.0	281	12	AAW11956	Fb-Fb-truncated (6
299	7	2.0	169	15	AAW51655	Osteogenic fusion	372	7	2.0	282	22	AAW55373	Novel human DNA-bi
300	7	2.0	169	17	AAW85765	OPLA fusion protei	373	7	2.0	283	22	AAW18235	Human calcium tran
301	7	2.0	169	19	AAW44305	Human osteogenic f	374	7	2.0	284	10	AAW95689	Consensus osteogen
302	7	2.0	169	20	AAW43116	Osteogenic protein	375	7	2.0	284	10	AAW95647	COP5 gene product.

376	7	2.0	286	17	AAW03566	Mycobacterium tube	449	7	2.0	405	4	AAP30202	Sequence encoded b
377	7	2.0	288	21	AAV95986	Human zinc finger	450	7	2.0	406	4	AAP30203	Sequence encoded b
378	7	2.0	296	22	ABB65345	Drosophila melanog	451	7	2.0	407	23	ABB92968	Herbicidally activ
379	7	2.0	297	22	ABG27036	Novel human diagno	452	7	2.0	408	14	AAR44752	Osteogenic fusion
380	7	2.0	307	21	AG433954	Zea mays protein f	453	7	2.0	408	15	AAR51658	Osteogenic fusion
381	7	2.0	310	21	AA814326	Mycobacterium tube	454	7	2.0	408	17	AAR55768	OPD fusion proteol
382	7	2.0	317	14	AAR44750	Osteogenic fusion	455	7	2.0	408	19	AAW44308	Human osteogenic f
383	7	2.0	317	15	AAR51656	Osteogenic fusion	456	7	2.0	408	20	AAW43119	Osteogenic protein
384	7	2.0	317	19	AAR55766	OP1B fusion protei	457	7	2.0	408	20	AAW89685	Osteogenic fusion
385	7	2.0	317	19	AAW44306	Human osteogenic f	458	7	2.0	418	22	ABG03314	Novel human diagno
386	7	2.0	317	20	AAW43117	Osteogenic protein	459	7	2.0	419	22	AAR44754	Osteogenic fusion
387	7	2.0	318	22	AAW89683	Osteogenic fusion	460	7	2.0	419	17	AAR55770	Human osteogenic f
388	7	2.0	318	22	AAW56362	Propionibacterium	461	7	2.0	419	19	AAW44310	CMMP2B2 fusion pro
389	7	2.0	320	21	AAW20559	Arabidopsis thalia	462	7	2.0	419	20	AAW43121	CMMP2B fusion prot
390	7	2.0	322	22	AAU97002	Human CCAAT/enhanc	463	7	2.0	419	20	AAW89687	Osteogenic fusion
391	7	2.0	322	22	AAE11945	Human CCAAT/enhanc	464	7	2.0	421	19	AAW37376	Hepatitis C virus
392	7	2.0	324	21	AA814143	Bordetella pertuss	465	7	2.0	421	22	ABG67110	Drosophila melanog
393	7	2.0	325	17	AAW03565	Mycobacterium tube	466	7	2.0	424	20	AAW49148	Amino acid sequenc
394	7	2.0	325	21	AAV97281	Fibronectin attach	467	7	2.0	425	20	AAW49147	Amino acid sequenc
395	7	2.0	325	23	AAW50732	Mycobacterium tube	468	7	2.0	426	20	AAW49146	Amino acid sequenc
396	7	2.0	331	22	AB370820	Drosophila melanog	469	7	2.0	428	20	AAW5085	S. pneumoniae resp
397	7	2.0	332	18	AAW32418	Mycobacterium tube	470	7	2.0	428	20	AAW5087	S. pneumoniae resp
398	7	2.0	332	18	AAW32350	Mycobacterium tube	471	7	2.0	429	21	AAW5087	S. pneumoniae resp
399	7	2.0	332	19	AAW81683	M. tuberculosis im	472	7	2.0	429	21	AAW5087	S. pneumoniae resp
400	7	2.0	332	19	AAW64322	Mycobacterium tube	473	7	2.0	431	21	AAW5087	S. pneumoniae resp
401	7	2.0	332	20	AAW39083	M. tuberculosis an	474	7	2.0	431	21	AAW5087	S. pneumoniae resp
402	7	2.0	332	20	AAW39083	M. tuberculosis an	475	7	2.0	431	21	AAW5087	S. pneumoniae resp
403	7	2.0	332	22	AAW18945	M. tuberculosis re	476	7	2.0	437	20	AAW49244	N-terminal region
404	7	2.0	332	22	AAW18945	M. tuberculosis re	477	7	2.0	437	20	AAW49244	N-terminal region
405	7	2.0	337	21	AAW74311	Mycobacterium spec	478	7	2.0	437	20	AAW32180	N-terminal choline
406	7	2.0	342	23	AAE22547	Neisseria gonorrhe	479	7	2.0	437	20	AAW32180	N-terminal choline
407	7	2.0	345	12	AAW14408	CTAI-DD fusion pro	480	7	2.0	439	20	AAW49240	N-terminal choline
408	7	2.0	345	22	AAU97001	Nuclear factor C/E	481	7	2.0	439	20	AAW32179	N-terminal choline
409	7	2.0	345	22	AAE11944	Human CCAAT/enhanc	482	7	2.0	444	23	AAE24240	Human 23566 (carbo
410	7	2.0	345	22	AAU90968	Human CCAAT/enhanc	483	7	2.0	453	15	AAW3918	CD protein of Bran
411	7	2.0	345	23	AAW15441	Human transcriptio	484	7	2.0	477	22	ABW59024	Drosophila melanog
412	7	2.0	345	23	AAW15442	Human C/EBP-beta p	485	7	2.0	477	22	AAU18155	Novel human DNA-bi
413	7	2.0	345	23	AAW15443	Human C/EBP-beta p	486	7	2.0	478	22	ABG02907	Novel human diagno
414	7	2.0	345	23	AAW15444	Human C/EBP-beta p	487	7	2.0	484	14	AAW44751	Osteogenic fusion
415	7	2.0	345	23	AAW15445	Human C/EBP-beta p	488	7	2.0	484	15	AAW51657	Osteogenic fusion
416	7	2.0	345	23	AAW15450	Human C/EBP-beta m	489	7	2.0	484	19	AAW55767	OPIC fusion protei
417	7	2.0	345	23	AAW15451	Human C/EBP-beta m	490	7	2.0	484	19	AAW55767	OPIC fusion protei
418	7	2.0	345	23	AAW15452	Human C/EBP-beta p	491	7	2.0	484	20	AAW43118	Human osteogenic f
419	7	2.0	345	23	AAW15453	Human C/EBP-beta p	492	7	2.0	484	20	AAW89684	Osteogenic protein
420	7	2.0	345	23	AAW15454	Human C/EBP-beta m	493	7	2.0	508	16	AAW80631	Osteogenic fusion
421	7	2.0	345	23	AAU97259	Human C/EBP-beta m	494	7	2.0	512	22	ABW61369	Osteogenic fusion
422	7	2.0	345	23	AAU97260	Human C/EBP-beta p	495	7	2.0	569	16	AAW80632	Osteogenic fusion
423	7	2.0	345	23	AAU97261	Human C/EBP-beta p	496	7	2.0	574	22	AAW52322	H1 AMH-receptor
424	7	2.0	345	23	AAU97262	Human C/EBP-beta p	497	7	2.0	574	22	AAW52322	WASP homolog prote
425	7	2.0	345	23	AAU97263	Human C/EBP-beta p	498	7	2.0	574	22	AAW52322	WASP homolog prote
426	7	2.0	345	23	AAU97264	Human C/EBP-beta p	499	7	2.0	576	22	ABW61241	Amino acid sequenc
427	7	2.0	345	23	AAU97265	Human C/EBP-beta p	500	7	2.0	587	22	ABW61241	Drosophila melanog
428	7	2.0	345	23	AAU97266	Human C/EBP-beta p	501	7	2.0	593	19	AAW61241	Pseudomonas aerugi
429	7	2.0	345	23	AAU97267	Human C/EBP-beta p	502	7	2.0	593	19	AAW61241	Human blue-light p
430	7	2.0	345	23	AAW49182	Human C/EBP-beta p	503	7	2.0	594	22	ABW61362	Drosophila melanog
431	7	2.0	350	23	AAW85938	Human C/EBP-beta p	504	7	2.0	609	4	AAP30206	Sequence encoded b
432	7	2.0	350	23	AAW85938	Human C/EBP-beta p	505	7	2.0	617	22	AAU09073	Mouse sphingosine
433	7	2.0	350	23	AAW85938	Human C/EBP-beta p	506	7	2.0	631	22	AAW83274	Chlamydia trachoma
434	7	2.0	354	22	ABW62869	Arabidopsis thalia	507	7	2.0	631	22	AAW83274	Chlamydia trachoma
435	7	2.0	354	22	ABW62869	Arabidopsis thalia	508	7	2.0	631	22	AAW83274	Chlamydia trachoma
436	7	2.0	354	22	ABW62869	Arabidopsis thalia	509	7	2.0	631	22	AAW83274	Chlamydia trachoma
437	7	2.0	354	22	ABW62869	Arabidopsis thalia	510	7	2.0	631	22	AAW83274	Chlamydia trachoma
438	7	2.0	354	22	ABW62869	Arabidopsis thalia	511	7	2.0	631	22	AAW83274	Chlamydia trachoma
439	7	2.0	354	22	ABW62869	Arabidopsis thalia	512	7	2.0	631	22	AAW83274	Chlamydia trachoma
440	7	2.0	354	22	ABW62869	Arabidopsis thalia	513	7	2.0	631	22	AAW83274	Chlamydia trachoma
441	7	2.0	354	22	ABW62869	Arabidopsis thalia	514	7	2.0	631	22	AAW83274	Chlamydia trachoma
442	7	2.0	354	22	ABW62869	Arabidopsis thalia	515	7	2.0	631	22	AAW83274	Chlamydia trachoma
443	7	2.0	354	22	ABW62869	Arabidopsis thalia	516	7	2.0	631	22	AAW83274	Chlamydia trachoma
444	7	2.0	354	22	ABW62869	Arabidopsis thalia	517	7	2.0	631	22	AAW83274	Chlamydia trachoma
445	7	2.0	354	22	ABW62869	Arabidopsis thalia	518	7	2.0	631	22	AAW83274	Chlamydia trachoma
446	7	2.0	354	22	ABW62869	Arabidopsis thalia	519	7	2.0	631	22	AAW83274	Chlamydia trachoma
447	7	2.0	354	22	ABW62869	Arabidopsis thalia	520	7	2.0	631	22	AAW83274	Chlamydia trachoma
448	7	2.0	354	22	ABW62869	Arabidopsis thalia	521	7	2.0	631	22	AAW83274	Chlamydia trachoma

522	7	2.0	802	20	AA939033	M. tuberculosis fu	595	7	2.0	2665	22	AA666665	Human bone marrow
523	7	2.0	802	23	AAU74592	Antigenic fusion p	596	7	2.0	2665	22	AA666665	Peptide #967 encod
524	7	2.0	811	22	AB626661	Drosophila melanog	597	7	2.0	2665	22	AA666665	Peptide #987 encod
525	7	2.0	852	20	AA931246	Murine rALGDS prot	598	7	2.0	2665	22	AA666665	Peptide #941 encod
526	7	2.0	852	20	AA930948	Human E3 ubiquitin	599	7	2.0	2665	23	ABG36319	Human peptide enco
527	7	2.0	852	21	AA923176	Human rALGDS (hral	600	7	2.0	3192	22	AAE10128	Streptomyces nous
528	7	2.0	854	20	AA930949	Murine E3 ubiquiti	601	7	2.0	3266	21	AAE42491	Human ORFX ORF2255
529	7	2.0	883	22	AA980136	Human protein SEQ	602	7	2.0	3266	21	AAE42491	Drosophila melanog
530	7	2.0	903	20	AA937116	Protein involved i	603	7	2.0	3536	22	AB65480	Peptide sequence o
531	7	2.0	919	22	AA979152	Human polypeptide	604	6	1.7	8	22	AA931876	Human Leukocyte An
532	7	2.0	931	22	AA939815	Streptococcus poly	605	6	1.7	8	22	AA931876	p53 epitope B7 sup
533	7	2.0	937	23	ABP30468	Streptococcus poly	606	6	1.7	8	22	AA931876	p53 epitope B7 sup
534	7	2.0	948	23	ABP27191	Human macrophage c	607	6	1.7	8	22	AA931876	Tumour associated
535	7	2.0	972	23	AA979039	Colony stimulating	608	6	1.7	8	22	AA979039	Tumour associated
536	7	2.0	972	23	AA979039	Colony stimulating	609	6	1.7	8	22	AA979039	Antigenic peptide,
537	7	2.0	972	23	AA979039	Colony stimulating	610	6	1.7	9	21	AA979039	HLA binding peptid
538	7	2.0	972	23	AA979039	Colony stimulating	611	6	1.7	9	21	AA979039	Human Leukocyte An
539	7	2.0	972	23	AA979039	Colony stimulating	612	6	1.7	9	21	AA979039	p53 DR supermotif
540	7	2.0	972	23	AA979039	Colony stimulating	613	6	1.7	10	17	AA979039	Antigenic peptide,
541	7	2.0	972	23	AA979039	Colony stimulating	614	6	1.7	10	17	AA979039	p53 derived immuno
542	7	2.0	972	23	AA979039	Colony stimulating	615	6	1.7	10	22	AA979039	Human Leukocyte An
543	7	2.0	972	23	AA979039	Colony stimulating	616	6	1.7	10	22	AA979039	p53 epitope B7 sup
544	7	2.0	972	23	AA979039	Colony stimulating	617	6	1.7	10	22	AA979039	MUCL1 competition b
545	7	2.0	972	23	AA979039	Colony stimulating	618	6	1.7	10	22	AA979039	Tumour associated
546	7	2.0	975	22	AAE07144	Mutant murine Kit/	619	6	1.7	10	22	AA979039	Tumour associated
547	7	2.0	976	22	AAE07148	Human Kit/stem cel	620	6	1.7	10	22	AA979039	Residues 68-78 of
548	7	2.0	976	22	AAE07149	Mutant human Kit/s	621	6	1.7	11	14	AA979039	p53 derived HLA an
549	7	2.0	976	22	AAU00375	Human stem cell gr	622	6	1.7	11	14	AA979039	Antigenic peptide,
550	7	2.0	976	22	AAU00375	Bovine c-Kit bk-1	623	6	1.7	11	14	AA979039	Ribosome binding s
551	7	2.0	1016	22	AA938901	C. trachomatis CT8	624	6	1.7	11	23	AA938901	Ribosome binding s
552	7	2.0	1021	19	AA976192	Actinoplanes sp. a	625	6	1.7	11	23	AA938901	Portion of Bacillu
553	7	2.0	1021	23	AA949562	Actinoplanes sp. a	626	6	1.7	12	16	AA938901	Tripartite operon
554	7	2.0	1023	23	AA982954	Human homologue of	627	6	1.7	12	16	AA982954	Human peptide #198
555	7	2.0	1039	22	AB691116	Drosophila melanog	628	6	1.7	12	12	AA982954	"Hydrophobic tail"
556	7	2.0	1055	22	AB691116	Novel human diago	629	6	1.7	13	12	AA982954	Peptide analogue o
557	7	2.0	1058	22	AB691116	Human ovarian anti	630	6	1.7	13	15	AA982954	House dust mite al
558	7	2.0	1130	23	AB691116	Human aortic carbo	631	6	1.7	13	15	AA982954	Der HMW-map polype
559	7	2.0	1138	23	AAE22739	Human adipocyte en	632	6	1.7	13	23	AA982954	Sequence present i
560	7	2.0	1243	22	ABG21221	Novel human diago	633	6	1.7	14	19	AA982954	Human peptide #161
561	7	2.0	1265	23	AAE22546	CTAL-OVA-DD fusion	634	6	1.7	14	22	AA982954	Bacillus thuringie
562	7	2.0	1298	16	AA95937	Protein tyrosine-k	635	6	1.7	15	18	AA95937	Peptide resembling
563	7	2.0	1298	17	AA95937	Flt4 receptor tyro	636	6	1.7	15	21	AA95937	Oestrogen receptor
564	7	2.0	1298	21	AA95937	Amino acid sequenc	637	6	1.7	15	21	AA95937	p53 DR supermotif
565	7	2.0	1298	21	AA95937	Human Flt4 recepto	638	6	1.7	15	22	AA95937	Soybean diverged d
566	7	2.0	1298	21	AA95937	Human Flt4 recepto	639	6	1.7	15	22	AA95937	GHR binding H5 pep
567	7	2.0	1298	21	AA95937	Human Flt4 recepto	640	6	1.7	15	22	AA95937	GHR binding H5 pep
568	7	2.0	1298	21	AA95937	Human Flt4 recepto	641	6	1.7	15	22	AA95937	Human cytomagalovi
569	7	2.0	1298	21	AA95937	Human Flt4 recepto	642	6	1.7	15	22	AA95937	HHV8 ORF K8.1-der1
570	7	2.0	1363	21	AA95937	Human Flt4 recepto	643	6	1.7	15	22	AA95937	HHV8 ORF K8.1-der1
571	7	2.0	1363	21	AA95937	Human Flt4 recepto	644	6	1.7	15	22	AA95937	HHV8 ORF K8.1-der1
572	7	2.0	1363	21	AA95937	Human Flt4 recepto	645	6	1.7	15	22	AA95937	HHV8 ORF K8.1-der1
573	7	2.0	1363	21	AA95937	Human Flt4 recepto	646	6	1.7	15	22	AA95937	HHV8 ORF K8.1-der1
574	7	2.0	1406	21	AA95937	Human Flt4 recepto	647	6	1.7	15	22	AA95937	HHV8 ORF K8.1-der1
575	7	2.0	1444	22	ABG15667	Human ORFX ORF2680	648	6	1.7	15	22	AA95937	HHV8 ORF K8.1-der1
576	7	2.0	1464	22	ABG15667	Novel human diago	649	6	1.7	15	22	AA95937	HHV8 ORF K8.1-der1
577	7	2.0	1487	23	AA914351	Drosophila melanog	650	6	1.7	15	22	AA95937	Peptide derived fr
578	7	2.0	1487	23	AA914351	Equine herpesvirus	651	6	1.7	15	22	AA95937	Peptide fragment o
579	7	2.0	1487	23	AA914351	Equine herpesvirus	652	6	1.7	15	22	AA95937	Insert A to preven
580	7	2.0	1487	23	AA914351	Equine herpesvirus	653	6	1.7	15	22	AA95937	Human cytomagalovi
581	7	2.0	1487	23	AA914351	Equine herpesvirus	654	6	1.7	15	22	AA95937	Delta6-16.0(delta6
582	7	2.0	1618	13	AA927205	Human nestin. Hom	655	6	1.7	15	22	AA95937	Delta6-16.0(delta6
583	7	2.0	1618	15	AA927205	Human nestin. Hom	656	6	1.7	15	22	AA95937	Delta6-16.0(delta6
584	7	2.0	1618	15	AA927205	Human nestin. Hom	657	6	1.7	15	22	AA95937	Human cytomagalovi
585	7	2.0	1618	15	AA927205	Human nestin. Hom	658	6	1.7	15	22	AA95937	HHV8 ORF K8.1-der1
586	7	2.0	1693	22	AA938901	Nestin polypeptide	659	6	1.7	15	22	AA938901	Peptide fragment o
587	7	2.0	1909	22	ABG19127	Drosophila melanog	660	6	1.7	15	22	ABG19127	Peptide fragment o
588	7	2.0	2129	22	ABG15478	Novel human diago	661	6	1.7	15	22	ABG15478	Insert A to preven
589	7	2.0	2129	22	ABG15478	Novel human diago	662	6	1.7	15	22	ABG15478	Human cytomagalovi
590	7	2.0	2220	21	AA954003	Novel human diago	663	6	1.7	15	22	AA954003	Delta6-16.0(delta6
591	7	2.0	2220	21	AA954003	Novel human diago	664	6	1.7	15	22	AA954003	Delta6-16.0(delta6
592	7	2.0	2665	22	AB628314	Human peptide #965	665	6	1.7	15	22	AB628314	Human cytomagalovi
593	7	2.0	2665	22	AB628314	Peptide #996 encod	666	6	1.7	15	22	AB628314	Human cytomagalovi
594	7	2.0	2665	22	AA954270	Human brain expres	667	6	1.7	15	22	AA954270	HHV8 ORF K8.1-der1

668	6	1.7	32	14	AAR33089	Human cytomegalovi	741	6	1.7	73	22	AAM86639	Human immune/haema
669	6	1.7	33	21	AAB44695	Human secreted pro	742	6	1.7	74	19	AAW40436	Tobacco invertase
670	6	1.7	34	13	AAR27562	Insert B to preven	743	6	1.7	74	21	AAW91020	Mouse OBH protein
671	6	1.7	34	19	AAW48443	Human p53 proline-	744	6	1.7	74	22	AAU61732	Propionibacterium
672	6	1.7	34	21	AAW58504	HV8 ORF K8.1 biva	745	6	1.7	76	21	AAW54024	Human pancreatic c
673	6	1.7	35	14	AAR33083	Human cytomegalovi	746	6	1.7	76	22	AAU62682	Propionibacterium
674	6	1.7	35	21	AAW22929	Arabidopsis thalia	747	6	1.7	76	22	AAW54024	C glutamicum prote
675	6	1.7	38	21	AAW57714	Arabidopsis thalia	748	6	1.7	76	22	AAW54024	Plant SDF encoded
676	6	1.7	40	21	AAW57714	Arabidopsis thalia	749	6	1.7	78	21	AAW54024	Plant SDF encoded
677	6	1.7	41	14	AAR33090	Human cytomegalovi	750	6	1.7	78	21	AAW54024	Novel human diago
678	6	1.7	41	14	AAR33092	Human cytomegalovi	751	6	1.7	78	21	AAW54024	Human death domain
679	6	1.7	41	22	AAE03992	Peptide #2229 enco	752	6	1.7	81	22	AAE00215	Human ORFX protein
680	6	1.7	42	22	AAW42515	Peptide derived fr	753	6	1.7	81	22	AAE00215	Drosophila melanog
681	6	1.7	42	22	ABW29611	Peptide #2262 enco	754	6	1.7	83	22	ABW68958	Propionibacterium
682	6	1.7	42	22	ABW34793	Peptide #2299 enco	755	6	1.7	83	22	AAU44488	Arabidopsis thalia
683	6	1.7	42	22	ABW20208	Protein #2207 enco	756	6	1.7	85	22	AAU37573	Propionibacterium
684	6	1.7	42	22	AAW55591	Human brain expres	757	6	1.7	85	22	AAU59296	Arabidopsis thalia
685	6	1.7	42	22	AAW67977	Human bone marrow	758	6	1.7	85	22	AAW67977	Propionibacterium
686	6	1.7	42	22	AAW15795	Peptide #2229 enco	759	6	1.7	86	21	AAW12105	Human foetal prote
687	6	1.7	42	22	AAW28304	Peptide #2341 enco	760	6	1.7	86	21	AAW59180	Arabidopsis thalia
688	6	1.7	42	22	AAW03530	Peptide #2212 enco	761	6	1.7	87	22	AAW93410	Propionibacterium
689	6	1.7	42	23	ABG37514	Human peptide enco	762	6	1.7	87	22	ABW69259	Amino acid sequenc
690	6	1.7	43	20	AAW14020	YhdP repeat sequen	763	6	1.7	87	22	AAU60382	Drosophila melanog
691	6	1.7	49	22	AAW82269	Human immune/haema	764	6	1.7	88	21	AAW61758	Propionibacterium
692	6	1.7	50	23	ABP32396	Human ORF1369 prot	765	6	1.7	88	23	ABP32396	Arabidopsis thalia
693	6	1.7	50	23	ABP32754	Human ORF1727 prot	766	6	1.7	88	23	ABP32754	Human ORF2191 prot
694	6	1.7	51	14	AAR33091	Human cytomegalovi	767	6	1.7	89	19	AAW98257	Human ORF3334 prot
695	6	1.7	52	21	AAW05444	Arabidopsis thalia	768	6	1.7	89	22	ABW69259	H. pylori GHPO 176
696	6	1.7	52	21	AAW33693	Arabidopsis thalia	769	6	1.7	90	16	AAW80185	Drosophila melanog
697	6	1.7	53	22	AAW04413	Arabidopsis thalia	770	6	1.7	90	22	AAE10715	MSP1-derived poly
698	6	1.7	57	21	AAW19720	Human polypeptide	771	6	1.7	90	22	AAE10715	Human 4ST3GalT do
699	6	1.7	57	21	AAW61016	Arabidopsis thalia	772	6	1.7	92	21	AAW68986	Mouse 4ST3GalT do
700	6	1.7	57	22	AAU40796	Arabidopsis thalia	773	6	1.7	93	21	AAW58908	Amino acid sequenc
701	6	1.7	57	22	AAU66718	Propionibacterium	774	6	1.7	93	21	AAW58908	Breast and ovarian
702	6	1.7	58	22	ABW40042	Propionibacterium	775	6	1.7	93	22	ABW30898	Eucalyptus grandis
703	6	1.7	58	22	ABW24544	Peptide #7548 enco	776	6	1.7	93	22	ABW30898	Peptide #3549 enco
704	6	1.7	58	22	AAW60792	Protein #6543 enco	777	6	1.7	93	22	ABW21472	Peptide #3586 enco
705	6	1.7	58	22	AAW13467	Human brain expres	778	6	1.7	93	22	AAW56862	Protein #3471 enco
706	6	1.7	58	22	AAW19975	Human bone marrow	779	6	1.7	93	22	AAW69249	Human brain expres
707	6	1.7	58	22	AAW33665	Peptide #6409 enco	780	6	1.7	93	22	AAW69249	Peptide #3512 enco
708	6	1.7	58	22	AAW33665	Peptide #7702 enco	781	6	1.7	93	22	AAW17078	Peptide #3609 enco
709	6	1.7	58	22	AAW33665	Human peptide enco	782	6	1.7	93	22	AAW404779	Peptide #3461 enco
710	6	1.7	59	23	ABP11067	Human ORFX protein	783	6	1.7	93	23	ABW38859	Human peptide enco
711	6	1.7	62	21	AAW45407	Human secreted pro	784	6	1.7	95	21	AAW59219	Arabidopsis thalia
712	6	1.7	62	22	AAU66864	Propionibacterium	785	6	1.7	95	22	AAW59219	Arabidopsis thalia
713	6	1.7	62	22	AAU54552	Propionibacterium	786	6	1.7	95	22	AAW57703	Propionibacterium
714	6	1.7	63	21	AAW20090	Arabidopsis thalia	787	6	1.7	95	22	AAW57703	Human immune/haema
715	6	1.7	63	22	AAW03612	Human secreted pro	788	6	1.7	97	21	AAW37572	Arabidopsis thalia
716	6	1.7	63	22	AAW1132	Hepatitis B virus	789	6	1.7	97	21	AAW37572	Propionibacterium
717	6	1.7	64	23	AAE17026	Hepatitis B virus	790	6	1.7	97	21	AAW37572	Human immune/haema
718	6	1.7	64	23	AAE11025	Human ORFX protein	791	6	1.7	98	22	AAU43179	Propionibacterium
719	6	1.7	65	22	AAU48572	Propionibacterium	792	6	1.7	98	22	ABW69550	Drosophila melanog
720	6	1.7	65	23	ABP10274	Human ORFX protein	793	6	1.7	101	22	AAU65875	Propionibacterium
721	6	1.7	67	23	AAE17028	C-terminally trunc	794	6	1.7	102	21	AAW19117	Polypeptide isolat
722	6	1.7	68	21	AAW59221	Arabidopsis thalia	795	6	1.7	102	22	AAU49619	Propionibacterium
723	6	1.7	68	22	AAW84291	Human immune/haema	796	6	1.7	103	22	AAU63289	Propionibacterium
724	6	1.7	68	22	AAW81134	Hepatitis B virus	797	6	1.7	104	21	AAW37572	Human p53 A767/V12
725	6	1.7	68	23	ABP10544	Human ORFX protein	798	6	1.7	104	22	AAW01073	Propionibacterium
726	6	1.7	69	21	AAW59220	Arabidopsis thalia	799	6	1.7	104	22	AAW01073	Arabidopsis thalia
727	6	1.7	69	22	AAU17820	Novel human respir	800	6	1.7	105	16	AAW80084	Human polypeptide
728	6	1.7	70	9	AAW80077	Cytomegalovirus (C	801	6	1.7	105	16	AAW80084	Mouse derived heavy
729	6	1.7	70	21	AAW26198	Arabidopsis thalia	802	6	1.7	105	20	AAW38669	Mouse derived heavy
730	6	1.7	70	22	ABW02382	Novel human diago	803	6	1.7	105	21	AAW38669	Amino acid sequenc
731	6	1.7	71	22	AAO12538	P. funiculosus aci	804	6	1.7	105	21	AAW61014	Arabidopsis thalia
732	6	1.7	72	21	AAW24991	Human polypeptide	805	6	1.7	105	22	ABW25066	Novel human diago
733	6	1.7	72	21	AAW25096	Plant SDF encoded	806	6	1.7	107	16	AAW94314	Arabidopsis thalia
734	6	1.7	72	22	ABW67912	Plant SDF encoded	807	6	1.7	107	16	AAW94314	Mouse derived heavy
735	6	1.7	73	22	AAW64454	Drosophila melanog	808	6	1.7	109	22	ABW67747	Lactococcus lactis
736	6	1.7	72	22	ABW26938	Propionibacterium	809	6	1.7	109	22	AAW31460	Drosophila melanog
737	6	1.7	73	22	AAW26938	Novel human diago	810	6	1.7	109	22	AAW26938	Novel human secret
738	6	1.7	73	21	AAW42000	Arabidopsis thalia	811	6	1.7	111	22	AAW94756	Human protein sequ
739	6	1.7	73	21	AAW03301	Human secreted pro	812	6	1.7	111	23	ABW05668	Human ORFX protein
740	6	1.7	73	22	ABW68706	Drosophila melanog	813	6	1.7	113	19	AAW60153	M. vaccae antigen
						Novel human diago						AAW14900	M. vaccae antigen

814	1.7	6	1.7	113	20	AA336969	Amino acid sequenc
815	1.7	6	1.7	113	23	AA782777	Human RNA cyclase
816	1.7	6	1.7	113	23	AB73506	M vaccae GV-42 pro
817	1.7	6	1.7	114	7	AP60286	Sequence of pre-S(
818	1.7	6	1.7	114	10	AP94770	ayw pre-S1 sequenc
819	1.7	6	1.7	114	21	AA30585	A human variable 1
820	1.7	6	1.7	116	16	AA80187	MISPI-derived poly
821	1.7	6	1.7	116	16	AA80189	MISPI-derived poly
822	1.7	6	1.7	116	21	AA37425	Human secreted pro
823	1.7	6	1.7	116	21	AA37426	Human secreted pro
824	1.7	6	1.7	117	22	AA80206	Human autoantibody
825	1.7	6	1.7	117	22	AA32011	Novel human secret
826	1.7	6	1.7	118	21	AA53493	Human colon cancer
827	1.7	6	1.7	118	22	AA001269	Human polypeptide
828	1.7	6	1.7	119	21	AA73472	Human polypeptide
829	1.7	6	1.7	119	21	AA65432	Human secreted pro
830	1.7	6	1.7	119	22	AA65251	Human 5' ESR relat
831	1.7	6	1.7	120	22	AA43965	Propionibacterium
832	1.7	6	1.7	120	22	AA43965	Propionibacterium
833	1.7	6	1.7	121	22	AB27743	Novel human diagno
834	1.7	6	1.7	121	22	AA49170	Novel human diagno
835	1.7	6	1.7	121	22	AB52527	Escherichia coli p
836	1.7	6	1.7	121	22	AA002146	Human polypeptide
837	1.7	6	1.7	121	23	AA074499	Human polypeptide
838	1.7	6	1.7	122	21	AA61497	Human interleukin
839	1.7	6	1.7	122	22	AB68984	Arabidopsis thalia
840	1.7	6	1.7	122	22	AA22040	Drosophila melanog
841	1.7	6	1.7	122	22	AA81517	Human cardiovascular
842	1.7	6	1.7	122	22	AA51103	Human P27 protein.
843	1.7	6	1.7	122	22	AA591168	Human P27 gi/35184
844	1.7	6	1.7	122	23	AA017362	165 gene homologou
845	1.7	6	1.7	124	18	AA014562	Human P27. Homo s
846	1.7	6	1.7	124	21	AA612104	Streptococcus thalia
847	1.7	6	1.7	125	7	AP60285	Sequence of pre-S(
848	1.7	6	1.7	125	10	AP94769	adw Pre-S1 sequenc
849	1.7	6	1.7	125	20	AA90283	Human anti-GPIIb/I
850	1.7	6	1.7	125	22	AA673577	Human colon cancer
851	1.7	6	1.7	127	22	AA0011736	Human polypeptide
852	1.7	6	1.7	128	21	AA009850	Arabidopsis thalia
853	1.7	6	1.7	129	21	AA84495	Plant viral move
854	1.7	6	1.7	129	22	AA339842	Propionibacterium
855	1.7	6	1.7	130	21	AA35182	Barley Rarl fragme
856	1.7	6	1.7	130	23	AB08370	Ribosomal protein
857	1.7	6	1.7	131	18	AA014583	Streptococcus pneu
858	1.7	6	1.7	131	21	AA51671	Gene 1 human secre
859	1.7	6	1.7	131	21	AA51672	Human secreted pro
860	1.7	6	1.7	131	21	AA660290	Arabidopsis thalia
861	1.7	6	1.7	131	21	AA02851	Human secreted pro
862	1.7	6	1.7	131	22	AB66858	Drosophila melanog
863	1.7	6	1.7	131	22	AA009514	Human polypeptide
864	1.7	6	1.7	132	19	AA075070	Human secreted pro
865	1.7	6	1.7	132	23	AAU75352	Human octamer bind
866	1.7	6	1.7	132	22	AB60260	Human ovarian anti
867	1.7	6	1.7	133	22	AA043804	Propionibacterium
868	1.7	6	1.7	133	22	AA044998	Propionibacterium
869	1.7	6	1.7	133	22	AA044998	Human reproductive
870	1.7	6	1.7	133	22	AA025765	Human protein sequ
871	1.7	6	1.7	133	22	AA025765	Human protein sequ
872	1.7	6	1.7	133	22	AA025765	Human protein sequ
873	1.7	6	1.7	133	22	AA025765	Human protein sequ
874	1.7	6	1.7	133	23	AB648094	Human polypeptide
875	1.7	6	1.7	136	21	AA009937	Human polypeptide
876	1.7	6	1.7	136	21	AA013639	Arabidopsis thalia
877	1.7	6	1.7	136	21	AA013639	Arabidopsis thalia
878	1.7	6	1.7	136	21	AA013639	Arabidopsis thalia
879	1.7	6	1.7	137	22	AA01761	Human secreted pro
880	1.7	6	1.7	138	23	AB049190	Listeria monocytog
881	1.7	6	1.7	139	21	AA009936	Arabidopsis thalia
882	1.7	6	1.7	139	21	AA009936	Arabidopsis thalia
883	1.7	6	1.7	139	22	AA009936	Arabidopsis thalia
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 999 6 1.7 193 23 ABG39918  
 1000 6 1.7 193 23 ABP42335  
 1000 6 1.7 194 20 AAY49916

## ALIGNMENTS

RESULT 1  
 AAB18994  
 ID AAB18994 standard; Protein; 344 AA.  
 XX  
 AC AAB18994;

DT 08-FEB-2001 (first entry)

DE A P40 polypeptide of Klebsiella pneumoniae.

XX P40; membrane fraction; Gram-negative bacteria; anticancer;  
 KW immune response; mononuclear blood cell; tumour necrosis factor-alpha;  
 KW interleukin-12; antitumour; cancer.

XX Klebsiella pneumoniae.

XX WO200054790-A1.

XX 21-SEP-2000.

XX 15-MAR-2000; 2000WO-FR00623.

XX 15-MAR-1999; 99FR-0003154.

XX (FABR ) FABRE MEDICAMENT SA PIERRE.

XX Libon C, Corvaia N, Beck A, Bonnefoy J;

XX DR WPI: 2000-587477/55.  
 DR N-PSDB; AAA96568.  
 XX  
 PT Use of membrane fractions from Gram-negative bacteria as  
 PT immunostimulants for the treatment or prevention of cancer, increases  
 PT effect of e.g. chemotherapeutic agents -  
 XX  
 PS Claim 6; Page 27-28; 34pp; French.  
 XX  
 CC The present sequence represents a P40 polypeptide of Klebsiella  
 CC pneumoniae. The protein is found in the membrane fraction, and is used in  
 CC the method of the invention. The specification describes the use of a  
 CC membrane fraction from Gram-negative bacteria for the preparation of an  
 CC immunostimulating composition that can induce an anticancer immune  
 CC response. The membrane fraction not only stimulates proliferation of  
 CC human mononuclear blood cells (immunostimulation) but also induces  
 CC production of tumour necrosis factor-alpha and interleukin (IL)-12, which  
 CC are known to have antitumour activity, so that it improves the effects of  
 CC other co-administered anticancer treatments (chemotherapy or radiation).  
 CC The membrane fraction is used for treatment and prevention of cancer  
 CC (particularly of the bladder, prostate, colon or liver) and also  
 CC malignant melanomas.  
 XX  
 SQ Sequence 344 AA;  
 Query Match 100.0%; Score 344; DB 21; Length 344;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKAIFVLAAPKDNWTWYAGGKLGWSQYHDTGYGNGFONNNGPTRNDOLGAGATGGYQVN 60  
 DB 1 MKAIFVLAAPKDNWTWYAGGKLGWSQYHDTGYGNGFONNNGPTRNDOLGAGATGGYQVN 60  
 QY 61 PYLGFEMGYDNLGRMAYKSGVDNGAFKAQGVQLTAKLGYPTITDLDIYTRLGGMWRADS 120  
 DB 61 PYLGFEMGYDNLGRMAYKSGVDNGAFKAQGVQLTAKLGYPTITDLDIYTRLGGMWRADS 120  
 QY 121 KGNVASTGVSRSEHDTGVSVPFAGGVAVTRDTATRLLEYQWVNNIGDAGTVGTRPDNGM 180  
 DB 121 KGNVASTGVSRSEHDTGVSVPFAGGVAVTRDTATRLLEYQWVNNIGDAGTVGTRPDNGM 180  
 QY 181 LSLGVSYRFGQEDAAPVYAP 240  
 DB 181 LSLGVSYRFGQEDAAPVYAP 240  
 QY 241 TQLSNMDPKDGSAYVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGE 300  
 DB 241 TQLSNMDPKDGSAYVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGE 300  
 QY 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGVEVTPAG 344  
 DB 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGVEVTPAG 344  
 RESULT 2  
 AAB18804  
 ID AAB18804 standard; Protein; 344 AA.  
 XX  
 AC AAB18804;  
 XX  
 DT 22-JAN-2001 (first entry)  
 XX  
 DE A Klebsiella pneumoniae P40 polypeptide.  
 XX  
 KW P40 polypeptide; membrane fraction; antigen; haptens; immune response;  
 KW infectious disease; cancer; paramyxovirus infection;  
 KW respiratory syncytial virus; parainfluenza.  
 XX  
 OS Klebsiella pneumoniae.  
 XX  
 PN WO200054789-A1.  
 XX







DB 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKYKEVVTQAG 344

RESULT 6  
RAY93341  
ID AAY93341 standard; Protein; 344 AA.  
AC AAY93341;  
XX  
DT 04-SEP-2000 (first entry)  
DE Amino acid sequence of a Klebsiella P40 protein.  
XX  
KW P40 protein; outer membrane protein A; OmpA; antigen-presenting cell;  
KW dendritic cell; antigen delivery; immune response; cancer;  
KW tumour-associated antigen; autoimmune disease; allergy; graft rejection;  
KW cardiovascular disease; central nervous system disease; inflammation;  
KW infection; immune deficiency.  
OS Klebsiella pneumoniae.  
XX  
FN WO200027432-A1.  
PD 18-MAY-2000.  
XX  
PF 08-NOV-1999; 99WO-FR02734.  
XX  
PR 06-NOV-1998; 98FR-0014007.  
XX  
PA (FABR ) FABRE MEDICAMENT SA PIERRE.  
XX  
PI Bonnefoy J, Lecoanet S, Aubry J, Jeannin P, Baussant T;  
XX  
DR WPI; 2000-387342/33.  
DR N-PSDB; AA15498.  
XX  
PT Use of enterobacterial outer membrane protein A for delivering active  
PT substances, particularly immunogens for treating or preventing e.g.  
PT cancer, to antigen presenting cells  
XX  
PS Claim 9; Page 28-29; 35pp; French.

XX The present sequence represents a P40 protein. The protein is an  
CC outer membrane protein A (OmpA). The protein is used in pharmaceutical  
CC compositions for specific targeting of an active substance to  
CC antigen-presenting cells (APCs), especially dendritic cells. OmpA binds  
CC specifically to APCs and is internalised by them (in contrast to other  
CC protein carriers such as tetanus toxoid). The OmpA protein is used to  
CC deliver an antigen or hapten to modify (specifically to improve) an  
CC immune response, especially for treatment or prevention of cancers  
CC (particularly those that express a associated-antigen),  
CC autoimmune disease, allergy, graft rejection, cardiovascular or  
CC central nervous system diseases, inflammation, infection or immune  
CC deficiency.  
XX

SQ Sequence 344 AA;  
Query Match 100.0%; Score 344; DB 21; Length 344;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKAIFVLAAPKDNNTWYAGKLGWSQYHDTGYGNGFQNNNGPTRNDQLGAGFGGYQVN 60  
DB 1 MKAIFVLAAPKDNNTWYAGKLGWSQYHDTGYGNGFQNNNGPTRNDQLGAGFGGYQVN 60  
QY 61 PYLGFEMGYDWLGRMAYKGSVDNGAFKAGQVLTAKLGPITDLDIYTRLGGMWWRADS 120  
DB 61 PYLGFEMGYDWLGRMAYKGSVDNGAFKAGQVLTAKLGPITDLDIYTRLGGMWWRADS 120  
QY 121 KGNVASTGVSRSSEHTGTGSPFAGGVENAVTRDTATRELYQWVNNIGDAGVGTTRPDNGM 180  
DB 121 KGNVASTGVSRSSEHTGTGSPFAGGVENAVTRDTATRELYQWVNNIGDAGVGTTRPDNGM 180

QY 181 LSLGVSYRFGQEDAAPVAPAPAPAPAPATKHFHTLKSDVLFNFNKATLKPEGQALDQLY 240  
DB 181 LSLGVSYRFGQEDAAPVAPAPAPAPAPATKHFHTLKSDVLFNFNKATLKPEGQALDQLY 240  
QY 241 TOLSNMDDPKGSASVVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGE 300  
DB 241 TOLSNMDDPKGSASVVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGE 300  
QY 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKYKEVVTQAG 344  
DB 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKYKEVVTQAG 344

RESULT 7  
AAG63698  
ID AAG63698 standard; Protein; 344 AA.  
XX  
AC AAG63698;  
XX  
DT 29-OCT-2001 (first entry)  
XX  
DE Amino acid sequence of an outer membrane protein A, P40.  
XX  
KW Outer membrane protein A; P40; antigen presenting cell; vaccine;  
KW antiviral; antibacterial; anticancer; autoimmune disease; inflammation;  
KW graft rejection; cardiovascular disease; immune deficiency.  
XX  
OS Klebsiella pneumoniae.  
XX  
FN FR2803302-A1.  
PD 06-JUL-2001.  
XX  
PF 04-JAN-2000; 2000FR-0000070.  
XX  
PR 04-JAN-2000; 2000FR-0000070.  
XX  
PA (FABR ) FABRE MEDICAMENT SA PIERRE.  
XX  
PI Baussant T, Jeannin P, Delneste Y, Lawny F, Bonnefoy JY;  
XX  
DR WPI; 2001-427232/46.  
DR N-PSDB; AAH74731.  
XX

PT Preparing purified polypeptide soluble in absence of detergent, useful  
PT for modulating the immune system, e.g. in vaccines, by removal of  
PT detergent, denaturing and molecular sieving  
XX  
PS Claim 9; Page 24-25; 34pp; French.

XX The present sequence represents an outer membrane protein A (P40) of  
CC Klebsiella pneumoniae. The protein is soluble in aqueous solvent in  
CC absence of detergent. The specification describes a method for the  
CC preparation of this polypeptide. The P40 protein binds selectively to  
CC antigen-presenting cell, so provides targeting, proliferation and/or  
CC expression of molecules by these cells. P40 is used, alone or as an  
CC adjuvant, to produce therapeutic compositions that are soluble in  
CC absence of detergent, especially when formulated with an antigen or  
CC hapten for modulating the host's immune system. Especially, it is used  
CC to prepare vaccines, especially antiviral, antibacterial or anticancer  
CC (e.g. against human immune deficiency virus, respiratory syncytial virus,  
CC measles, mumps, tuberculosis etc.), but also against fungi, parasites,  
CC autoimmune diseases, graft rejection, cardiovascular disease,  
CC inflammation and immune deficiency.  
XX

SQ Sequence 344 AA;  
Query Match 100.0%; Score 344; DB 22; Length 344;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKAIFVLAAPKDNNTWYAGKLGWSQYHDTGYGNGFQNNNGPTRNDQLGAGFGGYQVN 60  
DB 1 MKAIFVLAAPKDNNTWYAGKLGWSQYHDTGYGNGFQNNNGPTRNDQLGAGFGGYQVN 60

Db	1	MKAIFVNLNAPKDNWTYAGGLGWSQYHDTGYNGFQNNNGPTRNDQLCAGAGFGVQVN	60
QY	61	PYLGEMGYDMLGRMAYKGSVDNGAFKAQGVQLTAKLGYPTDDLDLYTLGGWVRADS	120
Db	61	PYLGEMGYDMLGRMAYKGSVDNGAFKAQGVQLTAKLGYPTDDLDLYTLGGWVRADS	120
QY	121	KGNVASTGVSRSEHDTGVSVPFAGVGEMVATRDITATLEYQWNNIGDAGTVGTRPDNGM	180
Db	121	KGNVASTGVSRSEHDTGVSVPFAGVGEMVATRDITATLEYQWNNIGDAGTVGTRPDNGM	180
QY	181	LSLGSVSYRFGQEDAAPVVPAPAPAPAPAVATKHFTLKSVDLNFENKATLXPEGQALDQLY	240
Db	181	LSLGSVSYRFGQEDAAPVVPAPAPAPAPAVATKHFTLKSVDLNFENKATLXPEGQALDQLY	240
QY	241	TQLSNMMDPKDGSVVYLVGTVDRIGSEAVNLOLSEKRAQSVVDYLVAKGIPAGKISARGMGE	300
Db	241	TQLSNMMDPKDGSVVYLVGTVDRIGSEAVNLOLSEKRAQSVVDYLVAKGIPAGKISARGMGE	300
QY	301	SNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKYEVVTQAP	344
Db	301	SNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKYEVVTQAP	344

RESULT 8	
AAB67770	
ID	AAB67770 standard; Protein; 344 AA.
XX	
AC	
AAB67770;	
XX	
DT	11-JUN-2001 (first entry)
XX	
XX	Amino acid sequence of an outer membrane protein A (OmpA) P40.
DE	
XX	
KW	Outer membrane protein A; OmpA; P40; enterobacteria; nasal composition;
KW	respiratory syncytial virus; RSV; RSV infection; lung; respiratory tract;
KW	vaccine.
XX	
OS	Klebsiella pneumoniae.
XX	
XX	WO200121203-A1.
PN	
XX	
XX	29-MAR-2001.
PD	
XX	
PF	22-SEP-2000; 2000WO-FR02626.
XX	
PR	23-SEP-1999; 99FR-0011888.
XX	
XX	(FABR ) FABRE MEDICAMENT SA PIERRE.
PA	
XX	
PI	Corvaiea N, Goestch L;
XX	
DR	WPI; 2001-257929/26.
DR	N-PSDB; AAF80152.
XX	
XX	Vaccine against respiratory syncytial virus, comprises enterobacterial
PT	outer membrane protein and viral immunogen, provides protective
PT	response throughout the respiratory tract
XX	
PS	Claim 3; Page 28-29; 39pp; French.

The present sequence represents an outer membrane protein A (OmpA), designated P40. Enterobacterium OmpA proteins, associated with an immunogenic peptide from respiratory syncytial virus (RSV), are used to prepare a nasal composition that induces a protective response, against RSV infection. In the upper and lower (lung) respiratory tract, OmpA potentiates the immune response to some immunogenic peptides, eliminating the need for adjuvants. The method is useful for producing vaccines for prevention or treatment of RSV infections.

Query Match	100.0%;	Score 344;	DB 22;	Length 344;
Best Local Similarity	100.0%;	Pred. No. 0;		

Matches	344;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;																																															
QY	1	MKAIFV	LN	AA	PK	DNTW	YAG	KL	GW	SO	YH	TG	FV	GN	GF	QNN	GP	TR	ND	Q	L	G	A	F	G	G	Y	Q	V	N	60																									
Db	1	MKAIFV	LN	AA	PK	DNTW	YAG	KL	GW	SO	YH	TG	FV	GN	GF	QNN	GP	TR	ND	Q	L	G	A	F	G	G	Y	Q	V	N	60																									
QY	61	PYLGF	EM	G	Y	D	W	L	G	R	M	A	Y	K	G	S	V	D	N	G	A	F	K	A	O	G	V	L	T	A	K	L	G	Y	P	I	T	D	D	L	I	D	I	T	R	L	G	M	Y	R	A	D	S	120		
Db	61	PYLGF	EM	G	Y	D	W	L	G	R	M	A	Y	K	G	S	V	D	N	G	A	F	K	A	O	G	V	L	T	A	K	L	G	Y	P	I	T	D	D	L	I	D	I	T	R	L	G	M	Y	R	A	D	S	120		
QY	121	KGN	Y	A	S	T	G	V	S	R	S	E	H	D	T	G	V	S	P	F	A	G	V	E	N	A	V	T	R	D	I	A	T	R	L	E	Y	O	W	N	N	I	G	D	A	G	T	V	T	R	P	D	N	G	M	180
Db	121	KGN	Y	A	S	T	G	V	S	R	S	E	H	D	T	G	V	S	P	F	A	G	V	E	N	A	V	T	R	D	I	A	T	R	L	E	Y	O	W	N	N	I	G	D	A	G	T	V	T	R	P	D	N	G	M	180
QY	181	LSL	G	S	Y	S	R	F	G	Q	D	A	P	V	V	A	P	A	P	A	P	A	P	E	V	A	T	K	H	F	L	K	S	D	V	L	E	N	F	N	K	A	T	L	K	P	E	Q	O	A	L	D	O	L	Y	240
Db	181	LSL	G	S	Y	S	R	F	G	Q	D	A	P	V	V	A	P	A	P	A	P	A	P	E	V	A	T	K	H	F	L	K	S	D	V	L	E	N	F	N	K	A	T	L	K	P	E	Q	O	A	L	D	O	L	Y	240
QY	241	TQ	L	S	N	M	D	P	K	G	S	A	V	V	L	G	T	D	R	I	G	S	E	A	Y	N	Q	O	L	S	E	K	R	A	O	S	V																			

RESULT 9  
AAM48395  
ID AAM48395 standard; protein; 344 AA.  
XX AC  
XX AAM48395;  
XX DT 10-MAY-2002 (first entry)  
XX DE Klebsiella pneumoniae outer membrane protein, OmpA.  
XX KW OmpA; outer membrane protein; cytosstatic; cancer; tumour antigen.  
XX OS Klebsiella pneumoniae.  
XX PN W0200182959-A1.  
XX PD 08-NOV-2001.  
XX PF 03-MAY-2001; 2001WO-FR01348.  
XX PR 04-MAY-2000; 2000FR-0005702.  
XX PA (FABR ) FABRE MEDICAMENT SA PIERRE.  
XX PI Renno T, Invernizzi I, Bonnefoy J;  
XX WP1; 2002-066490/09.  
XX PT Composition, useful for treatment and prevention of cancer, also for  
PT detecting tumor antigens, comprises an outer membrane protein and tumor  
BT Lysate -  
PS Claim 5; Page 25-26; 32pp; French.

The present invention relates to a pharmaceutical composition, comprising an Outer Membrane protein (e.g. OmpA), associated with a lysate of autologous and/or heterologous tumour cells. The present sequence is one such OmpA from *Klebsiella pneumoniae*. The composition is useful for the treatment of cancers, particularly where associated with tumour antigens, and for detecting tumour antigens.

SQ · Sequence 344 AA;

```
Query Match      100.0%; Score 344; DB 23; Length 344;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

RESULT 10	
AAM47796	
ID	AAM47796 standard; protein; 344 AA.
XX	
AC	AAM47796;
XX	
DT	01-MAR-2002 (first entry)
XX	
DE	Klebsiella pneumoniae OmpA protein.
XX	
XX	OmpA; enterobacterium; antibacterial; antifungal; antiviral;
KW	antiparasitic; antimicrobial; infection.
XX	
OS	Klebsiella pneumoniae.
XX	
PN	W0200187326-A1.
XX	
PD	22-NOV-2001.
XX	
PF	16-MAY-2001; 2001WO-FR01490.
XX	
PR	16-MAY-2000; 2000FR-0006199.
XX	
PA	(FABR ) FABRE MEDICAMENT SA PIERRE.
XX	
PI	Jeannin P, Delneste Y, Baussant T;
XX	
DR	WPI; 2002-055641/07.
XX	
PT	Use of an enterobacterium OmpA protein for prophylactic and therapeutic
XX	treatment of viral, bacterial, fungal and parasitic infections
PS	Claim 8; Page 24-25; 33pp; French.
XX	
CC	The present sequence is OmpA protein from enterobacteria Klebsiella
XX	pneumoniae. OmpA protein can be used to prepare an antimicrobial
CC	pharmaceutical composition for mucosal delivery. The composition can be
XX	used for prophylactic and therapeutic treatment of viral, bacterial,
CC	fungal and parasitic infections.
XX	
SQ	Sequence 344 AA;
Query Match	100.0%; Score 344; DB 23; Length 344;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 344; Conservative	0; Mismatches 0; Indels 0; Gaps
QY	1 MKAIFVLNAPKONTWAGCKLGSQYHDTGTGVNGFQNNNGTFRNDLGAGAFGGYQVN 60

CC and zoonosis caused by Salmonella of the same serogroup. The carrier  
 CC proteins enhance the immunogenicity of the oligo- or polysaccharide  
 CC antigens. Inclusion of additional Salmonella capsule antigens, such as  
 CC the Vi antigen, increases the vaccine's efficacy against encapsulated  
 CC bacteria. The present sequence, protein LP40, is a preferred example of  
 CC a carrier protein which can be used in the immunocomplex. It is  
 CC obtained by recombinant expression of a modified *Klebsiella pneumoniae* I-145  
 CC p40 gene in *E. coli*.  
 XX  
 SQ Sequence 344 AA;

Query Match 99.4%; Score 342; DB 18; Length 344;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKAIFVLNAAKPDNTWYAGGKLGWSQYHDTGYGNGFQNNNGPTRNDQLGAGAFGGYQVN 60  
 DB 1 MKAIFVLNAAKPDNTWYAGGKLGWSQYHDTGYGNGFQNNNGPTRNDQLGAGAFGGYQVN 60  
 QY 61 PYLGFEMGYDMLGRMAYKGSVDNGAFKAQGVOLTAQKGYPTDLDIYTRLGGMVWRADS 120  
 DB 61 PYLGFEMGYDMLGRMAYKGSVDNGAFKAQGVOLTAQKGYPTDLDIYTRLGGMVWRADS 120  
 QY 121 KGNVASTGVSSEHDTGSPVFAGGVAVTRDIATRLLEYQWVNNIGDAGTVGTRPDNGM 180  
 DB 121 KGNVASTGVSSEHDTGSPVFAGGVAVTRDIATRLLEYQWVNNIGDAGTVGTRPDNGM 180  
 QY 181 LSLGVSRYFGQEDAAPVVPAP 240  
 DB 181 LSLGVSRYFGQEDAAPVVPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 240  
 QY 241 TQLSNMDPKDGSVAVLGYTRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGE 300  
 DB 241 TQLSNMDPKDGSVAVLGYTRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGE 300  
 QY 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGKEVVTQP 342  
 DB 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGKEVVTQP 342

RESULT 12  
 AAY44077  
 ID AAY44077 standard; Protein; 344 AA.  
 AC AAY44077;  
 DT 18-JAN-2000 (first entry)  
 XX K.pneumoniae OmpA protein.  
 DE Outer membrane protein; ompA; enterobacterium; *Klebsiella pneumoniae*;  
 KW immunity; mammal; antigen; haptens; infection; human; bovine;  
 KW respiratory syncytial virus; protective response.  
 XX *Klebsiella pneumoniae*.  
 OS  
 XX FR2776521-A1.  
 PN  
 XX 01-OCT-1999.  
 PD  
 XX 27-MAR-1998; 98FR-0003814.  
 PF  
 XX 27-MAR-1998; 98FR-0003814.  
 PR  
 XX (FABR) FABRE MEDICAMENT SA PIERRE.  
 PA  
 XX Andreoni C, Rauli I, Nguyen TN, Haeuw JF, Baussant T;  
 PI  
 XX WPI; 1999-583089/50.  
 DR  
 XX N-PSDB; AAZ30477.  
 XX  
 PT Immunogenic composition containing bacterial outer membrane protein  
 PT conjugated or fused to antigen or haptens, for nasal administration, to

PT protect against respiratory pathogens -  
 XX Claim 1; Page 17-18; 64pp; French.  
 PS  
 XX The invention relates to the use of a fragment of a bacterial membrane  
 CC protein, especially the outer membrane protein from an enterobacterium,  
 CC e.g. the OmpA protein from *Klebsiella pneumoniae*, in a composition for  
 CC nasal administration to improve immunity, in mammals, against an antigen  
 CC or haptens. The antigen or haptens is derived from bacteria and viruses  
 CC that cause respiratory infections e.g. the human or bovine respiratory  
 CC syncytial virus. This sequence corresponds to the OmpA protein from  
 CC *Klebsiella*. The antigens are shown in AAY44078-Y44149 (AAZ30478-330538  
 CC for coding sequences). The use of a membrane protein, from a species  
 CC other than that from which the antigen is derived, induces a protective  
 CC response against the antigen, even without an adjuvant, since most  
 CC adults will already be sensitized against the membrane protein, although  
 CC the membrane protein-antigen product will induce an anti-membrane  
 CC protein response even in subjects who are not pre-sensitized.  
 XX  
 SQ Sequence 344 AA;

Query Match 99.4%; Score 342; DB 20; Length 344;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKAIFVLNAAKPDNTWYAGGKLGWSQYHDTGYGNGFQNNNGPTRNDQLGAGAFGGYQVN 60  
 DB 1 MKAIFVLNAAKPDNTWYAGGKLGWSQYHDTGYGNGFQNNNGPTRNDQLGAGAFGGYQVN 60  
 QY 61 PYLGFEMGYDMLGRMAYKGSVDNGAFKAQGVOLTAQKGYPTDLDIYTRLGGMVWRADS 120  
 DB 61 PYLGFEMGYDMLGRMAYKGSVDNGAFKAQGVOLTAQKGYPTDLDIYTRLGGMVWRADS 120  
 QY 121 KGNVASTGVSSEHDTGSPVFAGGVAVTRDIATRLLEYQWVNNIGDAGTVGTRPDNGM 180  
 DB 121 KGNVASTGVSSEHDTGSPVFAGGVAVTRDIATRLLEYQWVNNIGDAGTVGTRPDNGM 180  
 QY 181 LSLGVSRYFGQEDAAPVVPAP 240  
 DB 181 LSLGVSRYFGQEDAAPVVPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 240  
 QY 241 TQLSNMDPKDGSVAVLGYTRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGE 300  
 DB 241 TQLSNMDPKDGSVAVLGYTRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGE 300  
 QY 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGKEVVTQP 342  
 DB 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGKEVVTQP 342

RESULT 13  
 AAG67743  
 ID AAG67743 standard; Protein; 344 AA.  
 AC AAG67743;  
 XX  
 DT 10-DEC-2001 (first entry)  
 XX Amino acid sequence of a *Klebsiella pneumoniae*.  
 DE  
 XX zwitterionic detergent; immune response; vaccine; IgA production;  
 KW IGG response; tumour; viral infection; bacterial infection;  
 KW parasitic infection.  
 XX  
 OS *Klebsiella pneumoniae*.  
 XX  
 XX FR2805163-A1.  
 PN  
 XX 24-AUG-2001.  
 PD  
 XX 21-FEB-2000; 2000FR-0002104.  
 PF  
 XX 21-FEB-2000; 2000FR-0002104.  
 PR



XX AAB67771;  
XX 11-JUN-2001 (first entry)  
XX Amino acid sequence of a fusion protein of P40 and RSV antigen.  
XX Outer membrane protein A; OmpA; P40; enterobacteria; nasal composition;  
XX RSV; RSV infection; lung; respiratory tract; vaccine.  
XX Synthetic.  
XX Klebsiella pneumoniae.  
XX Respiratory syncytial virus.  
XX WO200121203-A1.  
XX 29-MAR-2001.  
XX 22-SEP-2000; 2000WO-FR02626.  
XX 23-SEP-1999; 99FR-0011888.  
XX (FABR ) FABRE MEDICAMENT SA PIERRE.  
XX Corvatea N, Goestch L;  
XX WPI; 2001-257929/26.  
XX N-PSDB; AAF80153.

PT Vaccine against respiratory syncytial virus, comprises enterobacterial  
PT outer membrane protein and viral immunogen, provides protective  
PT response throughout the respiratory tract  
XX Example 2; Page 31-32; 39pp; French.  
XX The present sequence represents a fusion protein comprising a Klebsiella  
XX pneumoniae outer membrane protein A (OmpA) designated P40 and a  
XX respiratory syncytial virus (RSV) antigen. Enterobacterium OmpA proteins,  
XX associated with an immunogenic peptide from RSV are used to prepare  
XX a nasal composition that induces a protective response, against RSV  
XX infection in the upper and lower (lung) respiratory tract. OmpA  
XX potentiates the immune response to some immunogenic peptides,  
XX eliminating the need for adjuvants. The method is useful for producing  
XX vaccines for prevention or treatment of RSV infections.

SQ Sequence 452 AA;

Query Match 99.4%; Score 342; DB 22; Length 452;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MKAIFVLNAPKNTWYAGKLGHSQYHDTGFCYNGFQNNNGPTRNDQLGAGAFGGYQVN 60  
Db 1 MKAIFVLNAPKNTWYAGKLGHSQYHDTGFCYNGFQNNNGPTRNDQLGAGAFGGYQVN 60  
Qy 61 PYLGFEMGYDNLGRMAYKGSVDNGAFKAQGVQLTAKLGYPTDLDIYTRLGGMVWRADS 120  
Db 61 PYLGFEMGYDNLGRMAYKGSVDNGAFKAQGVQLTAKLGYPTDLDIYTRLGGMVWRADS 120  
Qy 121 KGNVASTGVSRSRSHDTCVSPVAGGVEMAVTRDIATPLEYQWNNIGDAGTGTTRPDNGM 180  
Db 121 KGNVASTGVSRSRSHDTCVSPVAGGVEMAVTRDIATPLEYQWNNIGDAGTGTTRPDNGM 180  
Qy 181 LSLGVSYRFGQEDAAPVAP 240  
Db 181 LSLGVSYRFGQEDAAPVAP 240  
Qy 241 TQLSNMDPKDGSVVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGE 300  
Db 241 TQLSNMDPKDGSVVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGE 300  
Qy 301 SNPVTGNTCDNVKARAALIDCLAPDRREVEIKYKEVVTQP 342  
|||||

Db 301 SNPVTGNTCDNVKARAALIDCLAPDRREVEIKYKEVVTQP 342  
Search completed: April 15, 2003, 08:55:13  
Job time : 64 secs



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OM protein - protein search, using sw model

Run on: April 15, 2003, 08:54:09 ; Search time 15 Seconds  
(without alignments)  
674.766 Million cell updates/sec

Title: US-09-831-061-2

Perfect score: 344

Sequence: 1 MKAIFVLNAPAKDNTYAGG.....DRRVEIEVKGYKEVITQPAG 344

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 5

Total number of hits satisfying chosen parameters: 6183

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued\_Patents\_AA.\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	335	97.4	335	4	US-08-836-500A-2
2	179	52.0	179	4	US-08-836-500A-4
3	72	20.9	72	4	US-08-836-500A-6
4	53	15.4	53	4	US-08-836-500A-8
5	10	2.9	359	1	US-08-457-9978-2
6	10	2.9	359	3	US-08-467-722A-2
7	9	2.6	338	1	US-08-210-394-1
8	9	2.6	594	3	US-08-826-964-2
9	8	2.3	26	3	US-08-920-610-10
10	8	2.3	100	6	5252466-19
11	8	2.3	165	1	US-07-956-700B-106
12	8	2.3	165	1	US-08-476-537-106
13	8	2.3	165	1	US-08-485-607-106
14	8	2.3	165	2	US-08-473-879-106
15	8	2.3	165	4	US-09-433-043B-106
16	8	2.3	170	4	US-09-433-043B-127
17	8	2.3	197	1	US-08-690-095-5
18	8	2.3	197	3	US-09-113-789-5
19	8	2.3	404	4	US-09-203-468A-8
20	8	2.3	498	4	US-09-107-734A-5
21	8	2.3	537	3	US-08-920-610-2
22	8	2.3	550	5	PCT-US93-03027-1
23	8	2.3	719	4	US-08-765-907A-15
24	8	2.3	805	4	US-09-513-783A-178
25	7	2.0	35	4	US-09-001-984C-11
26	7	2.0	35	4	US-09-001-984C-42
27	7	2.0	40	4	US-08-795-430-4
28	7	2.0	40	4	US-08-510-133A-8
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49	7	2.0	169	1	US-08-447-570-9
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55	7	2.0	172	2	US-08-449-700-17
56	7	2.0	172	2	US-08-449-699A-17
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63	7	2.0	286	4	US-09-132-528-4
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69	7	2.0	317	1	US-07-841-646-11
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73	7	2.0	317	2	US-08-449-699A-11
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81	7	2.0	325	4	US-08-875-494-2
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93	7	2.0	367	1	US-08-257-341-5
94	7	2.0	408	1	US-07-841-646-15
95	7	2.0	408	1	US-08-147-023-15
96	7	2.0	408	1	US-08-447-570-15
97	7	2.0	408	2	US-08-449-700-15
98	7	2.0	408	2	US-08-449-699A-15
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101	7	2.0	419	1	US-08-447-570-19	Sequence 19, Appl	174	6	1.7	29	4	US-08-894-139-12	Sequence 12, Appl
102	7	2.0	419	2	US-08-449-700-19	Sequence 19, Appl	175	6	1.7	30	1	US-08-460-874A-14	Sequence 14, Appl
103	7	2.0	419	2	US-08-449-699A-19	Sequence 19, Appl	176	6	1.7	30	2	US-08-388-883B-14	Sequence 14, Appl
104	7	2.0	421	4	US-09-020-846-68	Sequence 68, Appl	177	6	1.7	30	2	US-08-462-211A-14	Sequence 14, Appl
105	7	2.0	428	4	US-09-139-064-4	Sequence 2, Appl	178	6	1.7	31	1	US-08-460-874A-12	Sequence 12, Appl
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107	7	2.0	428	4	US-09-487-370-2	Sequence 2, Appl	180	6	1.7	31	2	US-08-388-883B-12	Sequence 12, Appl
108	7	2.0	428	4	US-09-487-370-2	Sequence 4, Appl	181	6	1.7	31	2	US-08-388-883B-13	Sequence 13, Appl
109	7	2.0	433	1	US-08-810-116-9	Sequence 9, Appl	182	6	1.7	31	4	US-08-462-211A-12	Sequence 12, Appl
110	7	2.0	433	1	US-07-930-548A-9	Sequence 9, Appl	183	6	1.7	31	4	US-08-462-211A-13	Sequence 13, Appl
111	7	2.0	437	2	US-08-810-116-10	Sequence 10, Appl	184	6	1.7	32	2	US-08-460-874A-15	Sequence 15, Appl
112	7	2.0	437	2	US-07-930-548A-10	Sequence 10, Appl	185	6	1.7	32	2	US-08-388-883B-15	Sequence 15, Appl
113	7	2.0	484	1	US-07-841-646-13	Sequence 13, Appl	186	6	1.7	32	4	US-08-462-211A-15	Sequence 15, Appl
114	7	2.0	484	1	US-08-147-023-13	Sequence 13, Appl	187	6	1.7	34	6	5514582-28	Patent No. 5514582
115	7	2.0	484	1	US-08-447-570-13	Sequence 13, Appl	188	6	1.7	35	1	US-08-460-874A-9	Sequence 9, Appl
116	7	2.0	484	1	US-08-449-700-13	Sequence 13, Appl	189	6	1.7	35	2	US-08-388-883B-9	Sequence 9, Appl
117	7	2.0	484	2	US-08-449-699A-13	Sequence 13, Appl	190	6	1.7	35	2	US-08-462-211A-9	Sequence 9, Appl
118	7	2.0	582	3	US-08-906-865-3	Sequence 3, Appl	191	6	1.7	36	2	US-08-388-883B-16	Sequence 16, Appl
119	7	2.0	582	3	US-09-129-668-3	Sequence 3, Appl	192	6	1.7	38	4	US-08-826-134-28	Sequence 28, Appl
120	7	2.0	593	3	US-08-964-268-2	Sequence 2, Appl	193	6	1.7	40	2	US-08-388-883B-1	Sequence 1, Appl
121	7	2.0	631	4	US-09-620-412C-325	Sequence 325, App	194	6	1.7	41	1	US-08-460-874A-16	Sequence 16, Appl
122	7	2.0	640	4	US-09-177-349-4	Sequence 4, Appl	195	6	1.7	41	1	US-08-460-874A-18	Sequence 18, Appl
123	7	2.0	652	4	US-09-072-596-350	Sequence 350, App	196	6	1.7	41	2	US-08-388-883B-18	Sequence 18, Appl
124	7	2.0	802	4	US-09-056-556-214	Sequence 214, App	197	6	1.7	41	4	US-08-462-211A-16	Sequence 16, Appl
125	7	2.0	802	4	US-09-072-596-209	Sequence 209, App	198	6	1.7	42	4	US-08-826-134-17	Sequence 17, Appl
126	7	2.0	802	4	US-09-072-596-346	Sequence 346, App	199	6	1.7	42	4	US-08-062-472B-47	Sequence 47, Appl
127	7	2.0	852	2	US-08-408-519-5	Sequence 5, Appl	200	6	1.7	51	1	US-08-460-874A-17	Sequence 17, Appl
128	7	2.0	852	2	US-09-070-060-3	Sequence 3, Appl	201	6	1.7	51	2	US-08-388-883B-17	Sequence 17, Appl
129	7	2.0	852	3	PCT-US95-03552-5	Sequence 5, Appl	202	6	1.7	51	2	US-08-462-211A-17	Sequence 17, Appl
130	7	2.0	854	2	US-09-070-060-4	Sequence 4, Appl	203	6	1.7	51	6	5198542-13	Patent No. 5198542
131	7	2.0	854	2	US-09-357-746-4	Sequence 4, Appl	204	6	1.7	51	6	US-08-209-747-16	Sequence 16, Appl
132	7	2.0	972	3	US-08-750-141A-2	Sequence 2, Appl	205	6	1.7	90	1	US-08-458-298-16	Sequence 16, Appl
133	7	2.0	972	3	US-08-750-141A-2	Sequence 2, Appl	206	6	1.7	90	1	US-09-334-601-23	Sequence 23, Appl
134	7	2.0	976	3	US-09-060-482-2	Sequence 1, Appl	207	6	1.7	90	4	US-09-334-601-24	Sequence 24, Appl
135	7	2.0	1158	4	US-08-222-616-33	Sequence 33, Appl	208	6	1.7	90	4	US-09-334-601-25	Sequence 25, Appl
136	7	2.0	1298	1	US-08-340-011-2	Sequence 2, Appl	209	6	1.7	90	4	US-08-997-080-140	Sequence 140, App
137	7	2.0	1298	1	US-08-901-710-2	Sequence 2, Appl	210	6	1.7	102	4	US-08-997-080-140	Sequence 140, App
138	7	2.0	1298	3	US-08-446-648-33	Sequence 33, Appl	211	6	1.7	113	2	US-09-095-855-140	Sequence 140, App
139	7	2.0	1298	5	PCT-US95-04228-33	Sequence 33, Appl	212	6	1.7	113	2	US-09-324-542-140	Sequence 140, App
140	7	2.0	1362	2	US-08-874-678-33	Sequence 33, Appl	213	6	1.7	113	4	US-08-480-173A-52	Sequence 52, Appl
141	7	2.0	1362	3	US-08-643-839-33	Sequence 33, Appl	214	6	1.7	113	4	US-08-484-408A-52	Sequence 52, Appl
142	7	2.0	1362	3	US-08-643-839-33	Sequence 33, Appl	215	6	1.7	113	4	US-08-209-747-18	Sequence 18, Appl
143	7	2.0	1362	3	US-08-348-886-33	Sequence 33, Appl	216	6	1.7	114	3	US-08-458-298-18	Sequence 18, Appl
144	7	2.0	1363	1	US-08-340-011-4	Sequence 4, Appl	217	6	1.7	116	1	US-08-487-748A-17	Sequence 17, Appl
145	7	2.0	1363	2	US-08-874-678-32	Sequence 32, Appl	218	6	1.7	116	1	US-08-966-444-3	Sequence 3, Appl
146	7	2.0	1363	3	US-08-643-839-32	Sequence 32, Appl	219	6	1.7	122	2	US-08-398-633-17	Sequence 17, Appl
147	7	2.0	1363	3	US-08-901-710-4	Sequence 4, Appl	220	6	1.7	122	3	US-08-829-525-17	Sequence 17, Appl
148	7	2.0	1363	4	US-09-348-886-32	Sequence 32, Appl	221	6	1.7	122	3	US-08-609-583A-17	Sequence 17, Appl
149	7	2.0	1368	2	US-08-874-678-34	Sequence 34, Appl	222	6	1.7	122	4	US-08-937-399-17	Sequence 17, Appl
150	7	2.0	1368	3	US-08-643-839-34	Sequence 34, Appl	223	6	1.7	122	4	US-09-310-367-17	Sequence 17, Appl
151	7	2.0	1368	4	US-09-348-886-34	Sequence 34, Appl	224	6	1.7	122	4	US-09-032-337-17	Sequence 17, Appl
152	7	2.0	1618	1	US-07-853-913-4	Sequence 4, Appl	225	6	1.7	125	3	US-08-480-173A-50	Sequence 50, Appl
153	6	1.7	6	4	US-08-748-073-2	Sequence 2, Appl	226	6	1.7	125	3	US-08-484-408A-50	Sequence 50, Appl
154	6	1.7	6	4	US-08-766-596A-46	Sequence 46, Appl	227	6	1.7	140	4	US-09-091-725-45	Sequence 45, Appl
155	6	1.7	7	9	US-08-766-596A-45	Sequence 45, Appl	228	6	1.7	147	4	US-09-383-586-35	Sequence 35, Appl
156	6	1.7	7	5	PCT-US95-16415-19	Sequence 19, Appl	229	6	1.7	162	1	US-08-460-874A-33	Sequence 33, Appl
157	6	1.7	11	11	PCT-US95-16415-18	Sequence 8, Appl	230	6	1.7	162	2	US-08-388-883B-33	Sequence 33, Appl
158	6	1.7	11	5	PCT-US95-16415-18	Sequence 18, Appl	231	6	1.7	162	4	US-08-462-211A-33	Sequence 33, Appl
159	6	1.7	12	1	US-08-460-874A-46	Sequence 46, Appl	232	6	1.7	170	2	US-09-068-1140A-2	Sequence 2, Appl
160	6	1.7	12	2	US-08-388-883B-46	Sequence 46, Appl	233	6	1.7	170	4	US-09-361-707-49	Sequence 49, Appl
161	6	1.7	12	4	US-08-462-211A-46	Sequence 46, Appl	234	6	1.7	173	4	US-09-068-140A-13	Sequence 13, Appl
162	6	1.7	12	4	US-09-027-998A-47	Sequence 47, Appl	235	6	1.7	174	2	US-08-683-262B-42	Sequence 42, Appl
163	6	1.7	13	4	US-09-292-225-29	Sequence 29, Appl	236	6	1.7	174	2	US-08-683-262B-43	Sequence 43, Appl
164	6	1.7	15	4	US-08-602-999A-309	Sequence 309, App	237	6	1.7	174	2	US-08-683-262B-45	Sequence 45, Appl
165	6	1.7	15	4	US-09-027-998A-3	Sequence 3, Appl	238	6	1.7	174	2	US-08-683-262B-46	Sequence 46, Appl
166	6	1.7	15	4	US-09-500-124-309	Sequence 309, App	239	6	1.7	174	2	US-08-683-262B-47	Sequence 47, Appl
167	6	1.7	18	4	US-08-990-888-25	Sequence 25, Appl	240	6	1.7	174	2	US-08-683-262B-48	Sequence 48, Appl
168	6	1.7	18	4	US-08-990-888-28	Sequence 28, Appl	241	6	1.7	174	2	US-08-683-262B-49	Sequence 49, Appl
169	6	1.7	18	4	US-08-990-888-65	Sequence 65, Appl	242	6	1.7	174	2	US-08-683-262B-50	Sequence 50, Appl
170	6	1.7	20	4	US-08-935-009A-5	Sequence 5, Appl	243	6	1.7	174	2	US-08-683-262B-51	Sequence 51, Appl
171	6	1.7	21	1	US-08-460-874A-35	Sequence 35, Appl	244	6	1.7	174	2	US-08-683-262B-52	Sequence 52, Appl
172	6	1.7	21	2	US-08-388-883B-35	Sequence 35, Appl	245	6	1.7	174	2	US-08-683-262B-53	Sequence 53, Appl
173	6	1.7	21	4	US-08-462-211A-35	Sequence 35, Appl	246	6	1.7	174	2	US-08-683-262B-54	Sequence 54, Appl

247	6	1.7	174	2	US-08-683-262B-50	Sequence 50, Appl	320	6	1.7	307	4	US-09-368-402-3	Sequence 3, Appl
248	6	1.7	174	2	US-08-683-262B-51	Sequence 51, Appl	321	6	1.7	314	1	US-08-040-753-2	Sequence 2, Appl
249	6	1.7	174	2	US-08-683-262B-52	Sequence 52, Appl	322	6	1.7	314	4	US-09-004-838-14	Sequence 14, Appl
250	6	1.7	174	2	US-08-683-262B-53	Sequence 53, Appl	323	6	1.7	315	4	US-09-720-817-3	Sequence 3, Appl
251	6	1.7	174	2	US-08-683-262B-54	Sequence 54, Appl	324	6	1.7	315	4	US-09-720-817-6	Sequence 6, Appl
252	6	1.7	174	2	US-08-683-262B-55	Sequence 55, Appl	325	6	1.7	316	2	US-08-842-842-7	Sequence 7, Appl
253	6	1.7	174	2	US-08-683-262B-56	Sequence 56, Appl	326	6	1.7	316	4	US-08-989-362-2	Sequence 2, Appl
254	6	1.7	174	2	US-08-683-262B-57	Sequence 57, Appl	327	6	1.7	316	4	US-09-052-521C-2	Sequence 2, Appl
255	6	1.7	174	2	US-08-683-262B-58	Sequence 58, Appl	328	6	1.7	319	4	US-08-983-035A-42	Sequence 42, Appl
256	6	1.7	174	3	US-08-480-173A-44	Sequence 44, Appl	329	6	1.7	327	4	US-09-134-001C-3471	Sequence 3471, Ap
257	6	1.7	174	3	US-08-480-173A-45	Sequence 45, Appl	330	6	1.7	330	1	US-08-118-270-19	Sequence 19, Appl
258	6	1.7	174	3	US-08-480-173A-48	Sequence 48, Appl	331	6	1.7	330	5	PCT-US93-08528-19	Sequence 19, Appl
259	6	1.7	174	3	US-08-484-408A-44	Sequence 44, Appl	332	6	1.7	331	2	US-08-997-080-182	Sequence 182, App
260	6	1.7	174	3	US-08-484-408A-45	Sequence 45, Appl	333	6	1.7	331	2	US-08-997-362-182	Sequence 182, App
261	6	1.7	174	3	US-08-484-408A-48	Sequence 48, Appl	334	6	1.7	331	4	US-09-095-855-182	Sequence 182, App
262	6	1.7	174	3	US-08-484-408A-52	Sequence 52, Appl	335	6	1.7	331	4	US-09-324-542-182	Sequence 182, App
263	6	1.7	174	4	US-09-361-707-42	Sequence 42, Appl	336	6	1.7	331	4	US-09-205-426-182	Sequence 182, App
264	6	1.7	174	4	US-09-361-707-43	Sequence 43, Appl	337	6	1.7	335	4	US-08-983-035A-44	Sequence 44, Appl
265	6	1.7	174	4	US-09-361-707-45	Sequence 45, Appl	338	6	1.7	336	3	US-09-095-153-2	Sequence 2, Appl
266	6	1.7	174	4	US-09-361-707-46	Sequence 46, Appl	339	6	1.7	340	2	US-08-446-875-16	Sequence 16, Appl
267	6	1.7	174	4	US-09-361-707-47	Sequence 47, Appl	340	6	1.7	342	1	US-08-096-182A-4	Sequence 4, Appl
268	6	1.7	174	4	US-09-361-707-48	Sequence 48, Appl	341	6	1.7	342	1	US-08-877-109-4	Sequence 4, Appl
269	6	1.7	174	4	US-09-361-707-50	Sequence 50, Appl	342	6	1.7	342	3	US-08-798-760-4	Sequence 4, Appl
270	6	1.7	174	4	US-09-361-707-51	Sequence 51, Appl	343	6	1.7	342	5	PCT-US94-08327-4	Sequence 4, Appl
271	6	1.7	174	4	US-09-361-707-52	Sequence 52, Appl	344	6	1.7	343	2	US-08-446-875-2	Sequence 2, Appl
272	6	1.7	174	4	US-09-361-707-53	Sequence 53, Appl	345	6	1.7	343	2	US-08-102-365G-2	Sequence 2, Appl
273	6	1.7	174	4	US-09-361-707-54	Sequence 54, Appl	346	6	1.7	347	4	US-09-039-046-2	Sequence 2, Appl
274	6	1.7	174	4	US-09-361-707-55	Sequence 55, Appl	347	6	1.7	350	4	US-09-161-241-9	Sequence 9, Appl
275	6	1.7	174	4	US-09-361-707-56	Sequence 56, Appl	348	6	1.7	353	4	US-08-983-035A-40	Sequence 40, Appl
276	6	1.7	174	4	US-09-361-707-57	Sequence 57, Appl	349	6	1.7	360	2	US-08-319-866-2	Sequence 2, Appl
277	6	1.7	174	4	US-09-361-707-62	Sequence 62, Appl	350	6	1.7	361	4	US-09-134-001C-3862	Sequence 3862, Ap
278	6	1.7	174	6	5204096-1	Patent No. 5204096	351	6	1.7	362	4	US-09-485-648-6	Sequence 6, Appl
279	6	1.7	174	6	5204096-2	Patent No. 5204096	352	6	1.7	362	4	US-09-503-565-6	Sequence 6, Appl
280	6	1.7	174	6	5204096-5	Patent No. 5204096	353	6	1.7	362	4	US-09-485-649-6	Sequence 6, Appl
281	6	1.7	175	1	5198542-6	Patent No. 5198542	354	6	1.7	363	1	US-08-096-182A-6	Sequence 6, Appl
282	6	1.7	182	4	US-09-134-001C-2842	Sequence 2842, Ap	355	6	1.7	363	2	US-08-877-109-6	Sequence 6, Appl
283	6	1.7	189	4	US-09-134-001C-3795	Sequence 3795, Ap	356	6	1.7	363	2	US-08-697-221-17	Sequence 17, Appl
284	6	1.7	191	3	US-08-928-361B-26	Sequence 26, Appl	357	6	1.7	363	2	US-08-697-221-18	Sequence 18, Appl
285	6	1.7	191	3	US-09-171-517B-8	Sequence 8, Appl	358	6	1.7	363	2	US-08-697-221-19	Sequence 19, Appl
286	6	1.7	197	4	US-09-112-248-2	Sequence 2, Appl	359	6	1.7	363	2	US-08-697-221-20	Sequence 20, Appl
287	6	1.7	218	1	US-08-463-115-52	Sequence 92, Appl	360	6	1.7	363	2	US-08-697-221-21	Sequence 21, Appl
288	6	1.7	218	1	US-08-463-115-92	Sequence 92, Appl	361	6	1.7	363	2	US-08-697-221-22	Sequence 22, Appl
289	6	1.7	219	1	US-08-463-115-91	Sequence 91, Appl	362	6	1.7	363	2	US-08-697-221-23	Sequence 23, Appl
290	6	1.7	219	1	US-08-465-388-91	Sequence 91, Appl	363	6	1.7	363	2	US-08-697-221-24	Sequence 24, Appl
291	6	1.7	223	4	US-09-171-461-11	Sequence 11, Appl	364	6	1.7	363	3	US-08-798-760-6	Sequence 6, Appl
292	6	1.7	233	1	US-08-607-269-23	Sequence 23, Appl	365	6	1.7	363	4	US-08-983-035A-26	Sequence 26, Appl
293	6	1.7	233	5	PCT-US95-04600-23	Sequence 23, Appl	366	6	1.7	363	5	PCT-US94-08327-6	Sequence 6, Appl
294	6	1.7	234	4	US-08-936-165A-517	Sequence 517, App	367	6	1.7	371	4	US-09-134-001C-4502	Sequence 4502, Ap
295	6	1.7	236	1	US-08-315-695-18	Sequence 18, Appl	368	6	1.7	371	4	US-09-814-951A-2	Sequence 2, Appl
296	6	1.7	241	4	US-08-823-120-1	Sequence 1, Appl	369	6	1.7	374	4	US-08-983-035A-28	Sequence 28, Appl
297	6	1.7	245	3	US-09-286-690-2	Sequence 2, Appl	370	6	1.7	374	4	US-09-134-001C-2939	Sequence 2939, Ap
298	6	1.7	251	1	US-08-209-747-8	Sequence 8, Appl	371	6	1.7	381	4	US-08-983-035A-36	Sequence 36, Appl
299	6	1.7	251	1	US-08-458-298-8	Sequence 8, Appl	372	6	1.7	382	2	US-08-504-265B-75	Sequence 75, Appl
300	6	1.7	253	4	US-08-983-035A-30	Sequence 30, Appl	373	6	1.7	386	4	US-09-413-814-12	Sequence 12, Appl
301	6	1.7	254	2	US-08-948-616-9	Sequence 9, Appl	374	6	1.7	386	1	US-09-331-924-9	Sequence 9, Appl
302	6	1.7	254	2	US-09-193-510-9	Sequence 9, Appl	375	6	1.7	389	1	US-08-105-483-216	Sequence 216, App
303	6	1.7	254	4	US-09-368-402-9	Sequence 9, Appl	376	6	1.7	389	1	US-08-105-483-219	Sequence 219, App
304	6	1.7	261	4	US-09-414-436-3	Sequence 3, Appl	377	6	1.7	389	1	US-08-709-209-216	Sequence 216, App
305	6	1.7	263	1	US-08-117-083-9	Sequence 9, Appl	378	6	1.7	389	1	US-08-709-209-219	Sequence 219, App
306	6	1.7	270	4	US-08-983-035A-32	Sequence 32, Appl	379	6	1.7	389	1	US-08-458-101-216	Sequence 216, App
307	6	1.7	280	4	US-09-720-817-1	Sequence 1, Appl	380	6	1.7	389	1	US-08-458-101-219	Sequence 219, App
308	6	1.7	294	3	US-08-996-139-11	Sequence 11, Appl	381	6	1.7	389	3	US-08-486-099-106	Sequence 106, App
309	6	1.7	294	4	US-08-995-659-11	Sequence 11, Appl	382	6	1.7	389	3	US-08-360-107A-116	Sequence 116, App
310	6	1.7	294	4	US-09-215-649A-11	Sequence 11, Appl	383	6	1.7	389	3	US-08-484-223B-106	Sequence 106, App
311	6	1.7	294	4	US-09-577-780-11	Sequence 11, Appl	384	6	1.7	389	3	US-09-919-597-106	Sequence 106, App
312	6	1.7	299	4	US-09-069-023-20	Sequence 20, Appl	385	6	1.7	389	3	US-08-475-668A-106	Sequence 106, App
313	6	1.7	300	3	US-08-765-856-2	Sequence 2, Appl	386	6	1.7	389	3	US-08-485-551A-106	Sequence 106, App
314	6	1.7	300	4	US-08-935-009A-2	Sequence 2, Appl	387	6	1.7	389	3	US-08-471-913A-106	Sequence 106, App
315	6	1.7	302	3	US-08-765-856-4	Sequence 4, Appl	388	6	1.7	389	4	US-08-485-264A-106	Sequence 106, App
316	6	1.7	302	4	US-08-935-009A-4	Sequence 4, Appl	389	6	1.7	389	4	US-08-474-349A-106	Sequence 106, App
317	6	1.7	303	3	US-08-928-361B-7	Sequence 7, Appl	390	6	1.7	390	1	US-08-347-792-15	Sequence 15, Appl
318	6	1.7	307	2	US-08-948-616-3	Sequence 3, Appl	391	6	1.7	390	1	US-08-431-357-15	Sequence 15, Appl
319	6	1.7	307	2	US-09-193-510-3	Sequence 3, Appl	392	6	1.7	390	4	US-08-392-542-3	Sequence 3, Appl

393	6	1.7	390	4	US-08-894-327-3	Sequence 3, Appl1	466	6	1.7	410	4	US-09-650-855-41	Sequence 41, Appl1
394	6	1.7	390	4	US-09-685-027-3	Sequence 3, Appl1	467	6	1.7	412	4	US-09-445-472-1	Sequence 1, Appl1
395	6	1.7	390	5	PCT-US95-15353-15	Sequence 15, Appl1	468	6	1.7	413	2	US-08-759-599-12	Sequence 12, Appl1
396	6	1.7	393	1	US-08-047-041A-25	Sequence 25, Appl1	469	6	1.7	413	2	US-08-759-599-12	Sequence 12, Appl1
397	6	1.7	393	1	US-08-047-041A-26	Sequence 26, Appl1	470	6	1.7	414	1	US-08-255-471-9	Sequence 9, Appl1
398	6	1.7	393	1	US-08-047-041A-27	Sequence 27, Appl1	471	6	1.7	428	4	US-08-403-797-2	Sequence 2, Appl1
399	6	1.7	393	1	US-08-047-041A-28	Sequence 28, Appl1	472	6	1.7	428	4	US-08-883-515-2	Sequence 2, Appl1
400	6	1.7	393	1	US-08-347-792-2	Sequence 2, Appl1	473	6	1.7	434	3	US-08-444-644-23	Sequence 23, Appl1
401	6	1.7	393	1	US-08-390-516C-6	Sequence 6, Appl1	474	6	1.7	434	3	US-08-444-644-31	Sequence 31, Appl1
402	6	1.7	393	1	US-08-390-516C-7	Sequence 7, Appl1	475	6	1.7	434	3	US-08-444-644-40	Sequence 40, Appl1
403	6	1.7	393	1	US-08-390-516C-8	Sequence 8, Appl1	476	6	1.7	434	3	US-08-444-644-46	Sequence 46, Appl1
404	6	1.7	393	1	US-08-390-516C-9	Sequence 9, Appl1	477	6	1.7	434	3	US-08-232-246A-23	Sequence 23, Appl1
405	6	1.7	393	1	US-08-431-357-2	Sequence 2, Appl1	478	6	1.7	434	4	US-08-232-246A-31	Sequence 31, Appl1
406	6	1.7	393	1	US-08-390-515A-6	Sequence 6, Appl1	479	6	1.7	434	4	US-08-232-246A-40	Sequence 40, Appl1
407	6	1.7	393	1	US-08-390-515A-7	Sequence 7, Appl1	480	6	1.7	434	4	US-08-232-246A-46	Sequence 46, Appl1
408	6	1.7	393	1	US-08-390-515A-8	Sequence 8, Appl1	481	6	1.7	437	1	US-08-135-119-2	Sequence 2, Appl1
409	6	1.7	393	1	US-08-390-515A-9	Sequence 9, Appl1	482	6	1.7	437	2	US-08-481-814A-7	Sequence 7, Appl1
410	6	1.7	393	2	US-08-795-006A-32	Sequence 32, Appl1	483	6	1.7	439	2	US-08-959-638-9	Sequence 9, Appl1
411	6	1.7	393	2	US-08-697-221-2	Sequence 2, Appl1	484	6	1.7	446	4	US-09-457-046B-74	Sequence 74, Appl1
412	6	1.7	393	2	US-08-697-221-3	Sequence 3, Appl1	485	6	1.7	456	1	US-08-624-125-20	Sequence 20, Appl1
413	6	1.7	393	2	US-08-697-221-4	Sequence 4, Appl1	486	6	1.7	460	1	US-08-342-411A-2	Sequence 2, Appl1
414	6	1.7	393	2	US-08-697-221-11	Sequence 11, Appl1	487	6	1.7	461	1	US-08-194-338-4	Sequence 4, Appl1
415	6	1.7	393	2	US-08-697-221-12	Sequence 12, Appl1	488	6	1.7	461	1	US-08-330-518-2	Sequence 2, Appl1
416	6	1.7	393	2	US-08-697-221-13	Sequence 13, Appl1	489	6	1.7	461	1	US-08-330-283-2	Sequence 2, Appl1
417	6	1.7	393	2	US-08-697-221-14	Sequence 14, Appl1	490	6	1.7	461	2	US-08-646-248-2	Sequence 2, Appl1
418	6	1.7	393	2	US-08-697-221-15	Sequence 15, Appl1	491	6	1.7	461	5	PCT-US95-13924-2	Sequence 2, Appl1
419	6	1.7	393	2	US-08-697-221-16	Sequence 16, Appl1	492	6	1.7	461	5	PCT-US95-13931-2	Sequence 2, Appl1
420	6	1.7	393	2	US-08-697-221-25	Sequence 25, Appl1	493	6	1.7	468	2	US-08-839-008-7	Sequence 7, Appl1
421	6	1.7	393	2	US-08-697-221-26	Sequence 26, Appl1	494	6	1.7	468	4	US-09-032-523-8	Sequence 8, Appl1
422	6	1.7	393	2	US-08-697-221-27	Sequence 27, Appl1	495	6	1.7	476	4	US-09-134-001C-4458	Sequence 4458, Ap
423	6	1.7	393	2	US-08-697-221-28	Sequence 28, Appl1	496	6	1.7	476	4	US-09-263-023-4	Sequence 4, Appl1
424	6	1.7	393	2	US-08-801-718-6	Sequence 6, Appl1	497	6	1.7	484	3	US-09-471-867-4	Sequence 4, Appl1
425	6	1.7	393	2	US-08-801-718-7	Sequence 7, Appl1	498	6	1.7	484	4	US-08-906-743-4	Sequence 4, Appl1
426	6	1.7	393	2	US-08-801-718-8	Sequence 8, Appl1	499	6	1.7	486	4	US-07-794-393-2	Sequence 2, Appl1
427	6	1.7	393	2	US-08-801-718-9	Sequence 9, Appl1	500	6	1.7	488	1	US-08-001-711-2	Sequence 2, Appl1
428	6	1.7	393	2	US-08-247-904B-12	Sequence 12, Appl1	501	6	1.7	488	3	US-09-165-042-1	Sequence 1, Appl1
429	6	1.7	393	2	US-08-675-631-1	Sequence 1, Appl1	502	6	1.7	488	3	US-08-704-711A-22	Sequence 22, Appl1
430	6	1.7	393	3	US-08-767-942A-23	Sequence 23, Appl1	503	6	1.7	488	4	US-09-521-220-22	Sequence 22, Appl1
431	6	1.7	393	4	US-08-392-542-2	Sequence 2, Appl1	504	6	1.7	488	4	US-09-391-104-31	Sequence 31, Appl1
432	6	1.7	393	4	US-09-184-073-32	Sequence 32, Appl1	505	6	1.7	489	4	US-08-448-489-11	Sequence 11, Appl1
433	6	1.7	393	4	US-08-328-673A-9	Sequence 9, Appl1	506	6	1.7	495	3	US-09-079-415-4	Sequence 4, Appl1
434	6	1.7	393	4	US-08-894-327-2	Sequence 2, Appl1	507	6	1.7	498	1	US-08-080-855-1	Sequence 1, Appl1
435	6	1.7	393	4	US-09-308-914-2	Sequence 2, Appl1	508	6	1.7	500	4	US-09-326-203A-17	Sequence 17, Appl1
436	6	1.7	393	4	US-09-305-914-3	Sequence 3, Appl1	509	6	1.7	505	1	US-08-221-750A-5	Sequence 5, Appl1
437	6	1.7	393	4	US-09-305-914-4	Sequence 4, Appl1	510	6	1.7	507	5	PCT-US93-08386-8	Sequence 8, Appl1
438	6	1.7	393	4	US-09-685-027-2	Sequence 2, Appl1	511	6	1.7	522	4	US-08-894-818B-3	Sequence 3, Appl1
439	6	1.7	393	4	US-09-417-278A-2	Sequence 2, Appl1	512	6	1.7	522	4	US-09-445-472-4	Sequence 4, Appl1
440	6	1.7	393	5	PCT-US95-15353-2	Sequence 2, Appl1	513	6	1.7	527	4	US-08-365-486A-26	Sequence 26, Appl1
441	6	1.7	394	4	US-08-134-001C-4834	Sequence 4834, Ap	514	6	1.7	527	4	US-09-126-109-10	Sequence 10, Appl1
442	6	1.7	394	4	US-09-081-975-4	Sequence 4, Appl1	515	6	1.7	527	4	US-08-880-342-26	Sequence 26, Appl1
443	6	1.7	396	2	US-09-061-337-12	Sequence 12, Appl1	516	6	1.7	527	4	US-08-583-035A-38	Sequence 38, Appl1
444	6	1.7	396	2	US-09-122-129-12	Sequence 12, Appl1	517	6	1.7	535	4	US-08-456-837-2	Sequence 2, Appl1
445	6	1.7	396	3	US-09-340-991-12	Sequence 12, Appl1	518	6	1.7	538	1	US-08-457-342-2	Sequence 2, Appl1
446	6	1.7	396	3	US-08-974-609-12	Sequence 12, Appl1	519	6	1.7	538	1	US-08-457-646A-2	Sequence 2, Appl1
447	6	1.7	396	4	US-09-242-859A-2	Sequence 2, Appl1	520	6	1.7	538	1	US-08-458-076A-2	Sequence 2, Appl1
448	6	1.7	396	4	US-09-242-859A-6	Sequence 6, Appl1	521	6	1.7	538	1	US-08-457-335A-2	Sequence 2, Appl1
449	6	1.7	396	4	US-09-549-098-10	Sequence 10, Appl1	522	6	1.7	538	2	US-08-729-214-2	Sequence 2, Appl1
450	6	1.7	396	4	US-09-549-098-16	Sequence 16, Appl1	523	6	1.7	538	2	US-08-729-214-24	Sequence 24, Appl1
451	6	1.7	398	1	US-08-471-791-20	Sequence 20, Appl1	524	6	1.7	538	3	US-09-028-934-2	Sequence 2, Appl1
452	6	1.7	398	5	PCT-US91-01746-20	Sequence 20, Appl1	525	6	1.7	538	3	US-09-028-934-24	Sequence 24, Appl1
453	6	1.7	398	5	US-08-839-008-5	Sequence 5, Appl1	526	6	1.7	539	4	US-09-036-987A-11	Sequence 11, Appl1
454	6	1.7	401	2	US-09-347-801-16	Sequence 16, Appl1	527	6	1.7	539	4	US-09-370-700-11	Sequence 11, Appl1
455	6	1.7	401	4	US-09-347-801-16	Sequence 16, Appl1	528	6	1.7	546	2	US-08-713-928B-4	Sequence 4, Appl1
456	6	1.7	402	2	US-09-061-337-10	Sequence 10, Appl1	529	6	1.7	552	4	US-08-557-006C-40	Sequence 4, Appl1
457	6	1.7	403	2	US-09-122-129-10	Sequence 10, Appl1	530	6	1.7	566	2	US-07-862-588B-4	Sequence 2, Appl1
458	6	1.7	403	3	US-09-340-991-10	Sequence 10, Appl1	531	6	1.7	576	3	US-08-948-564-16	Sequence 4, Appl1
459	6	1.7	403	3	US-09-340-991-10	Sequence 10, Appl1	532	6	1.7	577	1	US-09-183-266A-49	Sequence 49, Appl1
460	6	1.7	403	4	US-09-549-098-10	Sequence 10, Appl1	533	6	1.7	587	1	US-08-398-008A-2	Sequence 2, Appl1
461	6	1.7	403	4	US-09-549-098-10	Sequence 10, Appl1	534	6	1.7	587	2	US-08-893-333-2	Sequence 2, Appl1
462	6	1.7	408	1	US-08-127-278-4	Sequence 4, Appl1	535	6	1.7	605	4	US-09-105-058C-24	Sequence 24, Appl1
463	6	1.7	408	1	US-08-555-860-4	Sequence 4, Appl1	536	6	1.7	608	4	US-09-134-001C-3855	Sequence 3855, Ap
464	6	1.7	408	4	US-09-651-656-41	Sequence 41, Appl1	537	6	1.7				
465	6	1.7	410	4			538	6	1.7				

539	6	1.7	610	2	US-08-724-394A-5	Sequence 5, Appl1	612	6	1.7	652	3	US-08-996-441B-98	Sequence 98, Appl1
540	6	1.7	619	1	US-08-465-746-2	Sequence 2, Appl1	613	6	1.7	652	3	US-08-996-441B-108	Sequence 108, App
541	6	1.7	619	1	US-08-214-164-2	Sequence 2, Appl1	614	6	1.7	652	3	US-08-996-441B-110	Sequence 110, App
542	6	1.7	619	2	US-08-467-852A-3	Sequence 3, Appl1	615	6	1.7	652	3	US-08-996-441B-111	Sequence 111, App
543	6	1.7	619	2	US-08-246-630-2	Sequence 2, Appl1	616	6	1.7	652	3	US-08-996-441B-113	Sequence 113, App
544	6	1.7	619	2	US-08-247-491A-3	Sequence 3, Appl1	617	6	1.7	652	3	US-08-993-722A-2	Sequence 2, Appl1
545	6	1.7	619	2	US-08-319-795-2	Sequence 2, Appl1	618	6	1.7	652	3	US-08-993-722A-4	Sequence 4, Appl1
546	6	1.7	619	2	US-08-468-985-2	Sequence 2, Appl1	619	6	1.7	652	3	US-08-993-722A-6	Sequence 6, Appl1
547	6	1.7	619	3	US-08-312-949-2	Sequence 2, Appl1	620	6	1.7	652	3	US-08-993-722A-8	Sequence 8, Appl1
548	6	1.7	620	4	US-08-982-785A-10	Sequence 10, Appl1	621	6	1.7	652	3	US-08-993-722A-10	Sequence 10, Appl1
549	6	1.7	627	4	US-09-071-035-452	Sequence 452, App	622	6	1.7	652	3	US-08-993-722A-12	Sequence 12, Appl1
550	6	1.7	641	4	US-08-811-481-2	Sequence 2, Appl1	623	6	1.7	652	3	US-08-993-722A-14	Sequence 14, Appl1
551	6	1.7	644	1	US-07-828-788A-4	Sequence 4, Appl1	624	6	1.7	652	3	US-08-993-722A-16	Sequence 16, Appl1
552	6	1.7	644	1	US-08-072-281-2	Sequence 2, Appl1	625	6	1.7	652	3	US-08-993-722A-18	Sequence 18, Appl1
553	6	1.7	644	1	US-08-295-060-2	Sequence 2, Appl1	626	6	1.7	652	3	US-08-993-722A-20	Sequence 20, Appl1
554	6	1.7	644	1	US-08-759-446-2	Sequence 2, Appl1	627	6	1.7	652	3	US-08-993-722A-22	Sequence 22, Appl1
555	6	1.7	644	4	US-09-027-998A-2	Sequence 2, Appl1	628	6	1.7	652	3	US-08-993-722A-24	Sequence 24, Appl1
556	6	1.7	644	5	PCR-US92-11337-4	Sequence 4, Appl1	629	6	1.7	652	3	US-08-993-722A-26	Sequence 26, Appl1
557	6	1.7	645	1	US-08-295-060-4	Sequence 2, Appl1	630	6	1.7	652	3	US-08-993-722A-28	Sequence 28, Appl1
558	6	1.7	648	1	US-08-072-070-2	Sequence 2, Appl1	631	6	1.7	652	3	US-08-993-722A-30	Sequence 30, Appl1
559	6	1.7	648	1	US-08-469-434-2	Sequence 2, Appl1	632	6	1.7	652	3	US-08-993-722A-32	Sequence 32, Appl1
560	6	1.7	648	1	US-08-214-222-2	Sequence 2, Appl1	633	6	1.7	652	3	US-08-993-722A-34	Sequence 34, Appl1
561	6	1.7	648	1	US-08-467-852A-2	Sequence 2, Appl1	634	6	1.7	652	3	US-08-993-722A-36	Sequence 36, Appl1
562	6	1.7	648	2	US-08-468-718-2	Sequence 2, Appl1	635	6	1.7	652	3	US-08-993-722A-38	Sequence 38, Appl1
563	6	1.7	648	2	US-08-247-491A-2	Sequence 2, Appl1	636	6	1.7	652	3	US-08-993-722A-40	Sequence 40, Appl1
564	6	1.7	648	3	US-08-446-201-3	Sequence 3, Appl1	637	6	1.7	652	3	US-08-993-722A-42	Sequence 42, Appl1
565	6	1.7	649	3	US-08-996-441B-109	Sequence 109, App	638	6	1.7	652	3	US-08-993-722A-44	Sequence 44, Appl1
566	6	1.7	649	3	US-08-993-722A-109	Sequence 109, App	639	6	1.7	652	3	US-08-993-722A-46	Sequence 46, Appl1
567	6	1.7	649	3	US-08-993-170A-109	Sequence 109, App	640	6	1.7	652	3	US-08-993-722A-48	Sequence 48, Appl1
568	6	1.7	649	3	US-08-993-775B-109	Sequence 109, App	641	6	1.7	652	3	US-08-993-722A-50	Sequence 50, Appl1
569	6	1.7	651	3	US-08-996-441B-52	Sequence 52, Appl1	642	6	1.7	652	3	US-08-993-722A-54	Sequence 54, Appl1
570	6	1.7	651	3	US-08-996-441B-56	Sequence 56, Appl1	643	6	1.7	652	3	US-08-993-722A-60	Sequence 60, Appl1
571	6	1.7	651	3	US-08-996-441B-58	Sequence 58, Appl1	644	6	1.7	652	3	US-08-993-722A-62	Sequence 62, Appl1
572	6	1.7	651	3	US-08-993-722A-52	Sequence 52, Appl1	645	6	1.7	652	3	US-08-993-722A-64	Sequence 64, Appl1
573	6	1.7	651	3	US-08-993-722A-56	Sequence 56, Appl1	646	6	1.7	652	3	US-08-993-722A-66	Sequence 66, Appl1
574	6	1.7	651	3	US-08-993-170A-52	Sequence 52, Appl1	647	6	1.7	652	3	US-08-993-722A-68	Sequence 68, Appl1
575	6	1.7	651	3	US-08-993-170A-58	Sequence 58, Appl1	648	6	1.7	652	3	US-08-993-722A-108	Sequence 108, App
576	6	1.7	651	3	US-08-993-170A-56	Sequence 56, Appl1	649	6	1.7	652	3	US-08-993-722A-110	Sequence 110, App
577	6	1.7	651	3	US-08-993-170A-58	Sequence 58, Appl1	650	6	1.7	652	3	US-08-993-722A-111	Sequence 111, App
578	6	1.7	651	3	US-08-993-775B-52	Sequence 52, Appl1	651	6	1.7	652	3	US-08-993-722A-113	Sequence 113, App
579	6	1.7	651	3	US-08-993-775B-58	Sequence 58, Appl1	652	6	1.7	652	3	US-08-993-170A-2	Sequence 2, Appl1
580	6	1.7	651	3	US-08-993-775B-58	Sequence 58, Appl1	653	6	1.7	652	3	US-08-993-170A-4	Sequence 4, Appl1
581	6	1.7	652	3	US-08-996-441B-2	Sequence 2, Appl1	654	6	1.7	652	3	US-08-993-170A-6	Sequence 6, Appl1
582	6	1.7	652	3	US-08-996-441B-4	Sequence 4, Appl1	655	6	1.7	652	3	US-08-993-170A-8	Sequence 8, Appl1
583	6	1.7	652	3	US-08-996-441B-6	Sequence 6, Appl1	656	6	1.7	652	3	US-08-993-170A-10	Sequence 10, Appl1
584	6	1.7	652	3	US-08-996-441B-8	Sequence 8, Appl1	657	6	1.7	652	3	US-08-993-170A-12	Sequence 12, Appl1
585	6	1.7	652	3	US-08-996-441B-10	Sequence 10, Appl1	658	6	1.7	652	3	US-08-993-170A-14	Sequence 14, Appl1
586	6	1.7	652	3	US-08-996-441B-12	Sequence 12, Appl1	659	6	1.7	652	3	US-08-993-170A-16	Sequence 16, Appl1
587	6	1.7	652	3	US-08-996-441B-14	Sequence 14, Appl1	660	6	1.7	652	3	US-08-993-170A-18	Sequence 18, Appl1
588	6	1.7	652	3	US-08-996-441B-16	Sequence 16, Appl1	661	6	1.7	652	3	US-08-993-170A-20	Sequence 20, Appl1
589	6	1.7	652	3	US-08-996-441B-18	Sequence 18, Appl1	662	6	1.7	652	3	US-08-993-170A-22	Sequence 22, Appl1
590	6	1.7	652	3	US-08-996-441B-20	Sequence 20, Appl1	663	6	1.7	652	3	US-08-993-170A-24	Sequence 24, Appl1
591	6	1.7	652	3	US-08-996-441B-22	Sequence 22, Appl1	664	6	1.7	652	3	US-08-993-170A-26	Sequence 26, Appl1
592	6	1.7	652	3	US-08-996-441B-24	Sequence 24, Appl1	665	6	1.7	652	3	US-08-993-170A-28	Sequence 28, Appl1
593	6	1.7	652	3	US-08-996-441B-26	Sequence 26, Appl1	666	6	1.7	652	3	US-08-993-170A-30	Sequence 30, Appl1
594	6	1.7	652	3	US-08-996-441B-28	Sequence 28, Appl1	667	6	1.7	652	3	US-08-993-170A-32	Sequence 32, Appl1
595	6	1.7	652	3	US-08-996-441B-30	Sequence 30, Appl1	668	6	1.7	652	3	US-08-993-170A-34	Sequence 34, Appl1
596	6	1.7	652	3	US-08-996-441B-32	Sequence 32, Appl1	669	6	1.7	652	3	US-08-993-170A-36	Sequence 36, Appl1
597	6	1.7	652	3	US-08-996-441B-34	Sequence 34, Appl1	670	6	1.7	652	3	US-08-993-170A-38	Sequence 38, Appl1
598	6	1.7	652	3	US-08-996-441B-36	Sequence 36, Appl1	671	6	1.7	652	3	US-08-993-170A-40	Sequence 40, Appl1
599	6	1.7	652	3	US-08-996-441B-38	Sequence 38, Appl1	672	6	1.7	652	3	US-08-993-170A-42	Sequence 42, Appl1
600	6	1.7	652	3	US-08-996-441B-40	Sequence 40, Appl1	673	6	1.7	652	3	US-08-993-170A-44	Sequence 44, Appl1
601	6	1.7	652	3	US-08-996-441B-42	Sequence 42, Appl1	674	6	1.7	652	3	US-08-993-170A-46	Sequence 46, Appl1
602	6	1.7	652	3	US-08-996-441B-44	Sequence 44, Appl1	675	6	1.7	652	3	US-08-993-170A-48	Sequence 48, Appl1
603	6	1.7	652	3	US-08-996-441B-46	Sequence 46, Appl1	676	6	1.7	652	3	US-08-993-170A-50	Sequence 50, Appl1
604	6	1.7	652	3	US-08-996-441B-48	Sequence 48, Appl1	677	6	1.7	652	3	US-08-993-170A-54	Sequence 54, Appl1
605	6	1.7	652	3	US-08-996-441B-50	Sequence 50, Appl1	678	6	1.7	652	3	US-08-993-170A-60	Sequence 60, Appl1
606	6	1.7	652	3	US-08-996-441B-54	Sequence 54, Appl1	679	6	1.7	652	3	US-08-993-170A-62	Sequence 62, Appl1
607	6	1.7	652	3	US-08-996-441B-60	Sequence 60, Appl1	680	6	1.7	652	3	US-08-993-170A-64	Sequence 64, Appl1
608	6	1.7	652	3	US-08-996-441B-62	Sequence 62, Appl1	681	6	1.7	652	3	US-08-993-170A-66	Sequence 66, Appl1
609	6	1.7	652	3	US-08-996-441B-64	Sequence 64, Appl1	682	6	1.7	652	3	US-08-993-170A-68	Sequence 68, Appl1
610	6	1.7	652	3	US-08-996-441B-66	Sequence 66, Appl1	683	6	1.7	652	3	US-08-993-170A-68	Sequence 68, Appl1
611	6	1.7	652	3	US-08-996-441B-68	Sequence 68, Appl1	684	6	1.7	652	3	US-08-993-170A-98	Sequence 98, Appl1

685	6	1.7	652	3	US-08-993-170A-108	Sequence 108, App	758	6	1.7	803	2	US-08-611-928-10	Sequence 10, Appl
686	6	1.7	652	3	US-08-993-170A-110	Sequence 110, App	759	6	1.7	803	3	US-09-173-891-10	Sequence 10, Appl
687	6	1.7	652	3	US-08-993-170A-111	Sequence 111, App	760	6	1.7	803	4	US-09-076-137-12	Sequence 12, Appl
688	6	1.7	652	3	US-08-993-170A-113	Sequence 113, App	761	6	1.7	803	5	PCT-US92-03624-12	Sequence 12, Appl
689	6	1.7	652	3	US-08-993-775B-2	Sequence 2, Appl	762	6	1.7	808	1	US-08-471-251A-2	Sequence 2, Appl
690	6	1.7	652	3	US-08-993-775B-4	Sequence 4, Appl	763	6	1.7	811	4	US-09-199-637A-93	Sequence 93, Appl
691	6	1.7	652	3	US-08-993-775B-6	Sequence 6, Appl	764	6	1.7	873	2	US-08-912-129A-61	Sequence 61, Appl
692	6	1.7	652	3	US-08-993-775B-8	Sequence 8, Appl	765	6	1.7	961	5	PCT-US93-11725-4	Sequence 4, Appl
693	6	1.7	652	3	US-08-993-775B-10	Sequence 10, Appl	766	6	1.7	964	3	US-08-860-339-18	Sequence 18, Appl
694	6	1.7	652	3	US-08-993-775B-12	Sequence 12, Appl	767	6	1.7	964	4	US-09-403-618A-6	Sequence 6, Appl
695	6	1.7	652	3	US-08-993-775B-14	Sequence 14, Appl	768	6	1.7	1012	4	US-08-811-481-16	Sequence 16, Appl
696	6	1.7	652	3	US-08-993-775B-16	Sequence 16, Appl	769	6	1.7	1030	4	US-09-091-117-2	Sequence 2, Appl
697	6	1.7	652	3	US-08-993-775B-18	Sequence 18, Appl	770	6	1.7	1048	4	US-09-171-699-10	Sequence 10, Appl
698	6	1.7	652	3	US-08-993-775B-20	Sequence 20, Appl	771	6	1.7	1070	3	US-08-922-635-22	Sequence 22, Appl
699	6	1.7	652	3	US-08-993-775B-22	Sequence 22, Appl	772	6	1.7	1084	4	US-09-221-725A-3	Sequence 3, Appl
700	6	1.7	652	3	US-08-993-775B-24	Sequence 24, Appl	773	6	1.7	1147	1	US-08-131-365B-38	Sequence 38, Appl
701	6	1.7	652	3	US-08-993-775B-26	Sequence 26, Appl	774	6	1.7	1147	2	US-08-668-123-38	Sequence 38, Appl
702	6	1.7	652	3	US-08-993-775B-28	Sequence 28, Appl	775	6	1.7	1169	1	US-08-315-468-4	Sequence 4, Appl
703	6	1.7	652	3	US-08-993-775B-30	Sequence 30, Appl	776	6	1.7	1196	4	US-08-881-706-2	Sequence 2, Appl
704	6	1.7	652	3	US-08-993-775B-32	Sequence 32, Appl	777	6	1.7	1211	4	US-09-134-001C-4820	Sequence 4820, Ap
705	6	1.7	652	3	US-08-993-775B-34	Sequence 34, Appl	778	6	1.7	1214	2	US-08-231-193A-54	Sequence 54, Appl
706	6	1.7	652	3	US-08-993-775B-36	Sequence 36, Appl	779	6	1.7	1214	2	US-08-486-273A-54	Sequence 54, Appl
707	6	1.7	652	3	US-08-993-775B-38	Sequence 38, Appl	780	6	1.7	1214	2	US-08-480-474-54	Sequence 54, Appl
708	6	1.7	652	3	US-08-993-775B-40	Sequence 40, Appl	781	6	1.7	1214	3	US-08-940-086A-54	Sequence 54, Appl
709	6	1.7	652	3	US-08-993-775B-42	Sequence 42, Appl	782	6	1.7	1214	4	US-08-940-035A-54	Sequence 54, Appl
710	6	1.7	652	3	US-08-993-775B-44	Sequence 44, Appl	783	6	1.7	1214	4	US-08-935-105A-54	Sequence 54, Appl
711	6	1.7	652	3	US-08-993-775B-46	Sequence 46, Appl	784	6	1.7	1214	4	US-09-648-797-54	Sequence 54, Appl
712	6	1.7	652	3	US-08-993-775B-48	Sequence 48, Appl	785	6	1.7	1219	2	US-08-231-193A-50	Sequence 50, Appl
713	6	1.7	652	3	US-08-993-775B-50	Sequence 50, Appl	786	6	1.7	1219	2	US-08-486-273A-50	Sequence 50, Appl
714	6	1.7	652	3	US-08-993-775B-54	Sequence 54, Appl	787	6	1.7	1219	3	US-08-480-474-50	Sequence 50, Appl
715	6	1.7	652	3	US-08-993-775B-60	Sequence 60, Appl	788	6	1.7	1219	3	US-08-940-086A-50	Sequence 50, Appl
716	6	1.7	652	3	US-08-993-775B-62	Sequence 62, Appl	789	6	1.7	1219	4	US-08-940-035A-50	Sequence 50, Appl
717	6	1.7	652	3	US-08-993-775B-64	Sequence 64, Appl	790	6	1.7	1219	4	US-08-935-105A-50	Sequence 50, Appl
718	6	1.7	652	3	US-08-993-775B-66	Sequence 66, Appl	791	6	1.7	1219	4	US-09-648-797-50	Sequence 50, Appl
719	6	1.7	652	3	US-08-993-775B-68	Sequence 68, Appl	792	6	1.7	1231	2	US-08-231-193A-48	Sequence 48, Appl
720	6	1.7	652	3	US-08-993-775B-98	Sequence 98, Appl	793	6	1.7	1231	2	US-08-486-273A-48	Sequence 48, Appl
721	6	1.7	652	3	US-08-993-775B-108	Sequence 108, Appl	794	6	1.7	1231	3	US-08-480-474-48	Sequence 48, Appl
722	6	1.7	652	3	US-08-993-775B-110	Sequence 110, Appl	795	6	1.7	1231	3	US-08-940-086A-48	Sequence 48, Appl
723	6	1.7	652	3	US-08-993-775B-111	Sequence 111, Appl	796	6	1.7	1231	4	US-08-940-035A-48	Sequence 48, Appl
724	6	1.7	652	3	US-08-993-775B-113	Sequence 113, Appl	797	6	1.7	1231	4	US-08-935-105A-48	Sequence 48, Appl
725	6	1.7	652	5	PCT-US92-00040-2	Sequence 2, Appl	798	6	1.7	1231	4	US-09-648-797-48	Sequence 48, Appl
726	6	1.7	652	6	5187091-2	Patent No. 5187091	799	6	1.7	1236	2	US-08-231-193A-6	Sequence 6, Appl
727	6	1.7	653	3	US-08-996-441B-100	Sequence 100, App	800	6	1.7	1236	2	US-08-486-273A-6	Sequence 6, Appl
728	6	1.7	653	3	US-08-993-722A-100	Sequence 100, App	801	6	1.7	1236	3	US-08-480-474-6	Sequence 6, Appl
729	6	1.7	653	3	US-08-993-170A-100	Sequence 100, App	802	6	1.7	1236	3	US-08-940-086A-6	Sequence 6, Appl
730	6	1.7	653	3	US-08-993-775B-100	Sequence 100, App	803	6	1.7	1236	4	US-08-940-035A-6	Sequence 6, Appl
731	6	1.7	654	4	US-08-894-818B-35	Sequence 35, Appl	804	6	1.7	1236	4	US-08-935-105A-6	Sequence 6, Appl
732	6	1.7	654	4	US-09-445-472-16	Sequence 16, Appl	805	6	1.7	1236	4	US-09-648-797-6	Sequence 6, Appl
733	6	1.7	654	4	US-08-894-818B-5	Sequence 5, Appl	806	6	1.7	1239	1	US-08-026-138E-3	Sequence 3, Appl
734	6	1.7	686	4	US-08-982-785A-8	Sequence 8, Appl	807	6	1.7	1239	2	US-08-231-193A-52	Sequence 52, Appl
735	6	1.7	695	1	US-08-127-499A-23	Sequence 23, Appl	808	6	1.7	1239	2	US-08-486-273A-52	Sequence 52, Appl
736	6	1.7	695	1	US-08-482-847-23	Sequence 23, Appl	809	6	1.7	1239	3	US-08-480-474-52	Sequence 52, Appl
737	6	1.7	704	1	US-08-190-802A-62	Sequence 62, Appl	810	6	1.7	1239	3	US-08-940-086A-52	Sequence 52, Appl
738	6	1.7	704	1	US-08-188-582-5	Sequence 5, Appl	811	6	1.7	1239	4	US-08-940-035A-52	Sequence 52, Appl
739	6	1.7	704	1	US-08-646-715-5	Sequence 5, Appl	812	6	1.7	1239	4	US-08-935-105A-52	Sequence 52, Appl
740	6	1.7	704	2	US-08-308-818-3	Sequence 3, Appl	813	6	1.7	1239	4	US-09-648-797-52	Sequence 52, Appl
741	6	1.7	704	4	US-08-477-346-62	Sequence 62, Appl	814	6	1.7	1244	2	US-08-231-193A-46	Sequence 46, Appl
742	6	1.7	704	4	US-08-473-089-62	Sequence 62, Appl	815	6	1.7	1244	2	US-08-486-273A-46	Sequence 46, Appl
743	6	1.7	704	4	US-08-487-072A-62	Sequence 62, Appl	816	6	1.7	1244	3	US-08-480-474-46	Sequence 46, Appl
744	6	1.7	713	1	US-08-453-472-6	Sequence 6, Appl	817	6	1.7	1244	3	US-08-940-086A-46	Sequence 46, Appl
745	6	1.7	713	1	US-08-038-948-7	Sequence 7, Appl	818	6	1.7	1244	4	US-08-940-035A-46	Sequence 46, Appl
746	6	1.7	713	1	US-08-038-948-8	Sequence 8, Appl	819	6	1.7	1244	4	US-08-935-105A-46	Sequence 46, Appl
747	6	1.7	713	1	US-08-038-948-10	Sequence 10, Appl	820	6	1.7	1244	4	US-09-648-797-46	Sequence 46, Appl
748	6	1.7	713	1	US-08-453-952-6	Sequence 6, Appl	821	6	1.7	1313	4	US-09-071-035-450	Sequence 450, App
749	6	1.7	713	2	US-08-862-903-6	Sequence 6, Appl	822	6	1.7	1313	4	US-09-071-035-454	Sequence 454, App
750	6	1.7	726	4	US-08-134-001C-4266	Sequence 4266, Ap	823	6	1.7	1381	4	US-09-540-245A-16	Sequence 16, Appl
751	6	1.7	756	4	US-08-982-785A-2	Sequence 2, Appl	824	6	1.7	1381	4	US-08-826-134-4	Sequence 4, Appl
752	6	1.7	766	2	US-08-846-762-5	Sequence 5, Appl	825	6	1.7	1382	3	US-09-057-570-4	Sequence 2, Appl
753	6	1.7	802	4	US-09-156-316-1	Sequence 1, Appl	826	6	1.7	1384	4	US-08-826-134-2	Sequence 11, Appl
754	6	1.7	802	4	US-09-134-001C-3840	Sequence 3840, Ap	827	6	1.7	1402	4	US-09-004-838-11	Sequence 11, Appl
755	6	1.7	803	1	US-08-158-233-10	Sequence 10, Appl	828	6	1.7	1464	2	US-08-026-138E-1	Sequence 1, Appl
756	6	1.7	803	1	US-08-304-626-10	Sequence 10, Appl	829	6	1.7	1464	2	US-08-231-193A-11	Sequence 11, Appl
757	6	1.7	803	1	US-08-316-301A-12	Sequence 12, Appl	830	6	1.7	1464	2	US-08-486-273A-11	Sequence 11, Appl

831	6	1.7	1464	3	US-08-940-086A-11	Sequence 11, Appl	904	5	1.5	9	5	PCT-US95-00147-73	Sequence 73, Appl
832	6	1.7	1464	4	US-08-436-332B-10	Sequence 10, Appl	905	5	1.5	10	1	US-08-346-333-45	Sequence 45, Appl
833	6	1.7	1464	4	US-08-940-035A-11	Sequence 11, Appl	906	5	1.5	10	2	US-08-617-929-39	Sequence 39, Appl
834	6	1.7	1464	4	US-08-935-105A-11	Sequence 11, Appl	907	5	1.5	10	2	US-08-428-257A-26	Sequence 26, Appl
835	6	1.7	1464	4	US-09-648-797-11	Sequence 11, Appl	908	5	1.5	10	4	US-09-001-984C-78	Sequence 78, Appl
836	6	1.7	1657	3	US-09-057-570-2	Sequence 2, Appl	909	5	1.5	10	5	PCT-US91-07506-45	Sequence 45, Appl
837	6	1.7	1721	3	US-08-700-651-5	Sequence 5, Appl	910	5	1.5	11	2	US-08-748-021-22	Sequence 22, Appl
838	6	1.7	1721	3	US-08-928-361B-6	Sequence 6, Appl	911	5	1.5	11	2	US-08-748-021-23	Sequence 23, Appl
839	6	1.7	1802	3	US-09-322-478-18	Sequence 18, Appl	912	5	1.5	11	2	US-08-748-021-24	Sequence 24, Appl
840	6	1.7	1805	3	US-09-057-570-7	Sequence 7, Appl	913	5	1.5	11	2	US-08-748-021-25	Sequence 25, Appl
841	6	1.7	1837	3	US-08-928-361B-5	Sequence 5, Appl	914	5	1.5	11	2	US-08-748-021-26	Sequence 26, Appl
842	6	1.7	1996	2	US-08-804-227C-9	Sequence 9, Appl	915	5	1.5	11	2	US-08-748-021-48	Sequence 48, Appl
843	6	1.7	1996	2	US-08-804-198-3	Sequence 3, Appl	916	5	1.5	11	2	US-08-748-021-49	Sequence 49, Appl
844	6	1.7	2172	1	US-08-611-107-31	Sequence 31, Appl	917	5	1.5	11	2	US-08-748-021-50	Sequence 50, Appl
845	6	1.7	2183	3	US-08-746-111-5	Sequence 5, Appl	918	5	1.5	11	2	US-08-748-021-51	Sequence 51, Appl
846	6	1.7	2318	4	US-09-091-219-24	Sequence 24, Appl	919	5	1.5	11	2	US-08-748-021-52	Sequence 52, Appl
847	6	1.7	3077	6	5223423-2	Patent No. 5223423	920	5	1.5	11	3	US-08-974-297-22	Sequence 22, Appl
848	6	1.7	3567	2	US-07-642-734C-4	Sequence 4, Appl	921	5	1.5	11	3	US-08-974-297-23	Sequence 23, Appl
849	6	1.7	3567	3	US-08-439-009A-4	Sequence 4, Appl	922	5	1.5	11	3	US-08-974-297-24	Sequence 24, Appl
850	6	1.7	3724	2	US-08-804-227C-10	Sequence 10, Appl	923	5	1.5	11	3	US-08-974-297-25	Sequence 25, Appl
851	6	1.7	3724	2	US-08-804-198-4	Sequence 4, Appl	924	5	1.5	11	3	US-08-974-297-26	Sequence 26, Appl
852	6	1.7	4472	2	US-08-804-227C-2	Sequence 2, Appl	925	5	1.5	11	3	US-08-974-297-48	Sequence 48, Appl
853	5	1.5	5	4	US-08-766-596A-47	Sequence 47, Appl	926	5	1.5	11	3	US-08-974-297-49	Sequence 49, Appl
854	5	1.5	6	1	US-07-718-577-11	Sequence 11, Appl	927	5	1.5	11	3	US-08-974-297-50	Sequence 50, Appl
855	5	1.5	6	1	US-08-179-481-41	Sequence 41, Appl	928	5	1.5	11	3	US-08-974-297-51	Sequence 51, Appl
856	5	1.5	7	2	US-08-705-660-40	Sequence 40, Appl	929	5	1.5	11	3	US-08-974-297-52	Sequence 52, Appl
857	5	1.5	7	2	US-08-437-013-18	Sequence 18, Appl	930	5	1.5	11	6	5378464-19	Patent No. 5378464
858	5	1.5	7	2	US-08-437-013-20	Sequence 20, Appl	931	5	1.5	12	1	US-07-778-233B-63	Sequence 63, Appl
859	5	1.5	7	2	US-08-630-645-25	Sequence 25, Appl	932	5	1.5	12	1	US-07-963-321-63	Sequence 63, Appl
860	5	1.5	7	2	US-09-174-060-17	Sequence 17, Appl	933	5	1.5	12	1	US-08-290-641-63	Sequence 63, Appl
861	5	1.5	7	3	US-08-989-045-40	Sequence 40, Appl	934	5	1.5	12	1	US-08-548-540-63	Sequence 63, Appl
862	5	1.5	7	3	US-08-338-383-17	Sequence 17, Appl	935	5	1.5	12	2	US-08-406-330-35	Sequence 35, Appl
863	5	1.5	7	4	US-09-258-754-48	Sequence 48, App	936	5	1.5	12	2	US-08-737-085A-8	Sequence 8, Appl
864	5	1.5	7	4	US-09-042-107-428	Sequence 428, App	937	5	1.5	12	2	US-08-556-597-35	Sequence 35, Appl
865	5	1.5	7	4	US-08-766-596A-25	Sequence 25, Appl	938	5	1.5	12	2	US-08-630-645-24	Sequence 24, Appl
866	5	1.5	7	5	PCT-US96-10220-25	Sequence 25, Appl	939	5	1.5	12	2	US-08-836-561-36	Sequence 36, Appl
867	5	1.5	8	1	US-08-174-365A-32	Sequence 32, Appl	940	5	1.5	12	3	US-08-630-645-24	Sequence 24, Appl
868	5	1.5	8	1	US-08-290-301-74	Sequence 74, Appl	941	5	1.5	12	3	US-09-246-258-8	Sequence 8, Appl
869	5	1.5	8	2	US-08-769-745-32	Sequence 32, Appl	942	5	1.5	12	3	US-09-246-258-9	Sequence 9, Appl
870	5	1.5	8	4	US-08-910-820-21	Sequence 21, Appl	943	5	1.5	12	4	US-08-660-092-1	Sequence 1, Appl
871	5	1.5	8	4	US-09-013-598-74	Sequence 74, Appl	944	5	1.5	12	4	US-08-660-092-215	Sequence 215, App
872	5	1.5	8	4	US-08-766-596A-44	Sequence 44, Appl	945	5	1.5	12	4	US-09-532-106-8	Sequence 8, Appl
873	5	1.5	8	6	5200320-24	Patent No. 5200320	946	5	1.5	12	4	US-09-532-106-9	Sequence 9, Appl
874	5	1.5	9	1	US-08-178-570-73	Sequence 73, Appl	947	5	1.5	12	4	US-09-160-513-1	Sequence 1, Appl
875	5	1.5	9	2	US-08-646-981-2	Sequence 2, Appl	948	5	1.5	12	4	US-09-160-513-215	Sequence 215, App
876	5	1.5	9	2	US-08-340-283-67	Sequence 67, Appl	949	5	1.5	12	4	US-08-766-596A-24	Sequence 24, Appl
877	5	1.5	9	2	US-08-340-283-120	Sequence 120, App	950	5	1.5	12	4	US-08-839-666-9	Sequence 9, Appl
878	5	1.5	9	2	US-08-482-651-6	Sequence 121, App	951	5	1.5	12	4	PCT-US96-09809-63	Sequence 63, Appl
879	5	1.5	9	2	US-08-482-651-8	Sequence 6, Appl	952	5	1.5	12	5	PCT-US96-10220-24	Sequence 24, Appl
880	5	1.5	9	2	US-08-482-651-9	Sequence 9, Appl	953	5	1.5	12	5	US-08-486-057B-24	Sequence 24, Appl
881	5	1.5	9	2	US-08-482-651-20	Sequence 20, Appl	954	5	1.5	12	5	US-08-789-588-24	Sequence 24, Appl
882	5	1.5	9	2	US-08-482-651-26	Sequence 26, Appl	955	5	1.5	13	2	US-08-726-464B-58	Sequence 58, Appl
883	5	1.5	9	2	US-08-482-651-36	Sequence 36, Appl	956	5	1.5	13	2	US-08-660-092-2	Sequence 2, Appl
884	5	1.5	9	2	US-08-845-926-39	Sequence 39, Appl	957	5	1.5	13	4	US-09-100-930A-25	Sequence 25, Appl
885	5	1.5	9	3	US-08-369-643-73	Sequence 73, Appl	958	5	1.5	13	4	US-09-160-513-2	Sequence 2, Appl
886	5	1.5	9	4	US-09-171-705-70	Sequence 70, Appl	959	5	1.5	14	2	US-08-482-651-1	Sequence 1, Appl
887	5	1.5	9	4	US-08-660-092-9	Sequence 9, Appl	960	5	1.5	14	2	US-08-482-651-54	Sequence 54, Appl
888	5	1.5	9	4	US-08-660-092-11	Sequence 11, Appl	961	5	1.5	14	2	US-08-617-929-41	Sequence 41, Appl
889	5	1.5	9	4	US-08-660-092-12	Sequence 12, Appl	962	5	1.5	14	2	US-08-660-092-3	Sequence 3, Appl
890	5	1.5	9	4	US-08-660-092-23	Sequence 23, Appl	963	5	1.5	14	4	US-08-660-092-4	Sequence 4, Appl
891	5	1.5	9	4	US-08-660-092-29	Sequence 29, Appl	964	5	1.5	14	4	US-08-660-092-5	Sequence 5, Appl
892	5	1.5	9	4	US-08-660-092-39	Sequence 39, Appl	965	5	1.5	14	4	US-08-660-092-7	Sequence 7, Appl
893	5	1.5	9	4	US-08-660-092-59	Sequence 59, Appl	966	5	1.5	14	4	US-09-400-653A-40	Sequence 40, Appl
894	5	1.5	9	4	US-09-160-513-9	Sequence 9, Appl	967	5	1.5	14	4	US-09-059-646-1	Sequence 1, Appl
895	5	1.5	9	4	US-09-160-513-11	Sequence 11, Appl	968	5	1.5	14	4	US-09-160-513-3	Sequence 3, Appl
896	5	1.5	9	4	US-09-160-513-12	Sequence 12, Appl	969	5	1.5	14	4	US-09-160-513-4	Sequence 4, Appl
897	5	1.5	9	4	US-09-160-513-23	Sequence 23, Appl	970	5	1.5	14	4	US-09-160-513-7	Sequence 7, Appl
898	5	1.5	9	4	US-09-160-513-29	Sequence 29, Appl	971	5	1.5	14	4	US-09-160-513-219	Sequence 219, App
899	5	1.5	9	4	US-09-160-513-39	Sequence 39, Appl	972	5	1.5	14	4	US-09-160-513-224	Sequence 224, App
900	5	1.5	9	4	US-09-160-513-39	Sequence 39, Appl	973	5	1.5	14	4	US-09-638-202A-9	Sequence 9, App
901	5	1.5	9	4	US-09-351-296-39	Sequence 39, Appl	974	5	1.5	15	1	US-08-625-691-3	Sequence 3, Ar
902	5	1.5	9	4	US-08-766-596A-43	Sequence 43, Appl	975	5	1.5	15	2	US-08-408-858A-5	Sequence 5, Ar
903	5	1.5	9	4			976	5	1.5	15	2		







Query Match 2.9%; Score 10; DB 1; Length 359;  
Best Local Similarity 100.0%; Pred. No. 0.19;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Molecule Type: protein

QY 321 CLAPDRRVEI 330  
DB 344 CLAPDRRVEI 353

RESULT 6  
US-08-467-722A-2  
Sequence 2, Application US/08467722A  
Patent No. 6030626  
GENERAL INFORMATION:  
APPLICANT: Kollattukudy, P. E.  
TITLE OF INVENTION: Otitis Media Vaccine  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Calfee, Halter and Griswold  
STREET: Suite 1800 800 Superior Avenue  
CITY: Cleveland  
STATE: Ohio  
COUNTRY: U.S.A.  
ZIP: 44114-2688  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/457-997B  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Gollrick, Mary E.  
REGISTRATION NUMBER: 34,829  
REFERENCE/DOCKET NUMBER: 22727/00102  
TELEPHONE: (216) 622-8458  
TELEFAX: (216) 622-8458  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 359 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-457-997B-2  
Query Match 2.9%; Score 10; DB 1; Length 359;  
Best Local Similarity 100.0%; Pred. No. 0.19;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 321 CLAPDRRVEI 330  
DB 344 CLAPDRRVEI 353

RESULT 6  
US-08-467-722A-2  
Sequence 2, Application US/08467722A  
Patent No. 6030626  
GENERAL INFORMATION:  
APPLICANT: Kollattukudy, P. E.  
TITLE OF INVENTION: Otitis Media Vaccine  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Calfee, Halter and Griswold  
STREET: Suite 1800 800 Superior Avenue  
CITY: Cleveland  
STATE: Ohio  
COUNTRY: U.S.A.  
ZIP: 44114-2688  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467-722A  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Gollrick, Mary E.  
REGISTRATION NUMBER: 34,829  
REFERENCE/DOCKET NUMBER: 22727/00102  
TELEPHONE: (216) 622-8458  
TELEFAX: (216) 622-8458  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 359 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

US-08-467-722A-2  
Molecule Type: protein

Query Match 2.9%; Score 10; DB 3; Length 359;  
Best Local Similarity 100.0%; Pred. No. 0.19;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 321 CLAPDRRVEI 330  
DB 344 CLAPDRRVEI 353

RESULT 7  
US-08-210-394-1  
Sequence 1, Application US/08210394  
Patent No. 5770213  
GENERAL INFORMATION:  
APPLICANT: Zlotnick Dr., Gary W.  
TITLE OF INVENTION: Purified No. 5770213typable Haemophilus  
TITLE OF INVENTION: Influenzae p5 Protein as a Vaccine for No. 5770213typable  
TITLE OF INVENTION: Haemophilus Influenzae Strain  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Cyanamid Plaza  
CITY: Wayne  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07470-8426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/210,394  
FILING DATE: 07-MAR-1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Harrington, James J  
REFERENCE/DOCKET NUMBER: 32,144  
TELEPHONE: 201/831-3246  
TELEFAX: 201/831-3305  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 338 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein

US-08-210-394-1  
Query Match 2.6%; Score 9; DB 1; Length 338;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 LAPDRRVEI 330  
DB 324 LAPDRRVEI 332

RESULT 8  
US-08-826-964-2  
Sequence 2, Application US/08826964  
Patent No. 6033663  
GENERAL INFORMATION:  
APPLICANT: Ketcham, Catherine M.  
TITLE OF INVENTION: Nucleic Acids Encoding GDP-Fucose  
TITLE OF INVENTION: Pyrophosphorylase  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP

```
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/826,964
FILING DATE: 09-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/015,241
FILING DATE: 10-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 014137-0099100S
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 594 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-826-964-2

Query Match      2.6%; Score 9; DB 3; Length 594;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 AYNQQLSEK 274
DB 52 AYNQQLSEK 60

RESULT 9
US-08-920-610-10
; Sequence 10, Application US/08920610
; Patent No. 6015709
; GENERAL INFORMATION:
; APPLICANT: Natesan, Sridaran
; TITLE OF INVENTION: TRANSCRIPTIONAL ACTIVATORS, AND
; TITLE OF INVENTION: COMPOSITIONS AND USES RELATED THERETO
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/920,610
; FILING DATE: 27-AUG-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: APV-006.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
```

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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-920-610-10

Query Match      2.3%; Score 8; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 APAPAPAP 206
DB 16 APAPAPAP 23

RESULT 10
5252466-19
; Patent No. 5252466
; APPLICANT: CRONAN, JOHN E.
; TITLE OF INVENTION: FUSION PROTEINS HAVING A SITE FOR IN
; VIVO POST-TRANSLATION MODIFICATION AND METHODS OF MAKING AND
; PURIFYING THEM
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/525,568
; FILING DATE: 18-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 354,266
; FILING DATE: 19-MAY-1989
; SEQ ID NO:19;
; LENGTH: 100
; 5252466-19

Query Match      2.3%; Score 8; DB 6; Length 100;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 APAPAPAP 206
DB 9 APAPAPAP 16

RESULT 11
US-07-956-700B-106
; Sequence 106, Application US/07956700B
; Patent No. 5539092
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5539092th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/956,700B
; FILING DATE: 19921002
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5539092thrup
; REGISTRATION NUMBER: 33,268
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;; REFERENCE/DOCKET NUMBER: ARCD:058  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 1-312-744-0090  
;; TELEFAX: 1-312-755-4489  
;; INFORMATION FOR SEQ ID NO: 106:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 165 amino acids  
;; TYPE: Amino acid  
;; STRANDEDNESS: Single  
;; TOPOLOGY: Linear  
;; MOLECULE TYPE: Peptide  
US-07-956-700B-106

Query Match 2.3%; Score 8; DB 1; Length 165;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 APAPAP 206  
DB 74 APAPAP 81

## RESULT 12

US-08-476-537-106  
; Sequence 106, Application US/08476537  
; Patent No. 5756290

## GENERAL INFORMATION:

;; APPLICANT: Robert Haselkorn and Piotr Gornicki  
;; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA  
;; TITLE OF INVENTION: Carboxylase  
;; NUMBER OF SEQUENCES: 116

## CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Arnold, White & Durkee  
;; STREET: 321 No. 5756290th Clark Street  
;; CITY: Chicago  
;; STATE: Illinois  
;; COUNTRY: USA  
;; ZIP: 60610

## COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy Disk  
;; COMPUTER: IBM PC Compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: ASCII-DOS  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/476.537  
;; FILING DATE:

## CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/956,700  
;; FILING DATE: 10/21/92

## ATTORNEY/AGENT INFORMATION:

;; NAME: Thomas E. No. 5756290thrup  
;; REGISTRATION NUMBER: 33,268  
;; REFERENCE/DOCKET NUMBER: ARCD:058  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 1-312-744-0090

## INFORMATION FOR SEQ ID NO: 106:

;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 165 amino acids  
;; TYPE: Amino acid  
;; STRANDEDNESS: Single  
;; TOPOLOGY: Linear  
;; MOLECULE TYPE: Peptide  
US-08-476-537-106

Query Match 2.3%; Score 8; DB 1; Length 165;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 APAPAP 206  
DB 74 APAPAP 81

## RESULT 13

US-08-485-607-106  
; Sequence 106, Application US/08485607  
; Patent No. 5792627

## GENERAL INFORMATION:

;; APPLICANT: Robert Haselkorn and Piotr Gornicki  
;; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA  
;; TITLE OF INVENTION: Carboxylase  
;; NUMBER OF SEQUENCES: 116

## CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Arnold, White & Durkee  
;; STREET: 321 No. 5792627th Clark Street  
;; CITY: Chicago  
;; STATE: Illinois  
;; COUNTRY: USA  
;; ZIP: 60610

## COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy Disk  
;; COMPUTER: IBM PC Compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: ASCII-DOS  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/485,607  
;; FILING DATE: 07-JUN-1995

## CLASSIFICATION: 800

## PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 07/956,700  
;; FILING DATE: 10/21/92

## ATTORNEY/AGENT INFORMATION:

;; NAME: Thomas E. No. 5792627thrup  
;; REGISTRATION NUMBER: 33,268  
;; REFERENCE/DOCKET NUMBER: ARCD:058  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 1-312-744-0090

## INFORMATION FOR SEQ ID NO: 106:

;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 165 amino acids  
;; TYPE: Amino acid  
;; STRANDEDNESS: Single  
;; TOPOLOGY: Linear  
;; MOLECULE TYPE: Peptide  
US-08-485-607-106

Query Match 2.3%; Score 8; DB 1; Length 165;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 APAPAP 206  
DB 74 APAPAP 81

## RESULT 14

US-08-475-879-106  
; Sequence 106, Application US/08475879  
; Patent No. 5972644

## GENERAL INFORMATION:

;; APPLICANT: Robert Haselkorn and Piotr Gornicki  
;; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA  
;; TITLE OF INVENTION: Carboxylase  
;; NUMBER OF SEQUENCES: 116

## CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Arnold, White & Durkee  
;; STREET: 321 No. 5972644 5786170th Clark Street  
;; CITY: Chicago  
;; STATE: Illinois  
;; COUNTRY: USA  
;; ZIP: 60610

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII-DOS  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,879  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/956,700  
FILING DATE: 10/21/92  
ATTORNEY/AGENT INFORMATION:  
NAME: Thomas E. No. 5972644 5786170thrup  
REGISTRATION NUMBER: 33,268  
REFERENCE/DOCKET NUMBER: ARCD:058  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 1-312-744-0090  
TELEFAX: 1-312-755-4489  
INFORMATION FOR SEQ ID NO: 106:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 165 amino acids  
TYPE: Amino acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: Peptide  
US-08-475-879-106

Query Match 2.3%; Score 8; DB 2; Length 165;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 APAPAP 206  
Db 74 APAPAP 81

RESULT 15  
US-09-433-043B-106  
Sequence 106, Application US/09433043B  
Patent No. 6399342  
GENERAL INFORMATION:  
APPLICANT: HASELKORN, ROBERT  
APPLICANT: GORNICKI, PIOTR  
TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-COA CARBOXYLASE  
FILE REFERENCE: ARCD:338US  
CURRENT APPLICATION NUMBER: US/09/433,043B  
CURRENT FILING DATE: 1999-10-25  
PRIOR APPLICATION NUMBER: 08/475,879  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: 07/956,700  
PRIOR FILING DATE: 1992-10-02  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 106  
LENGTH: 165  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: Peptide  
US-09-433-043B-106

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Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 APAPAP 206  
Db 74 APAPAP 81

Search completed: April 15, 2003, 08:56:53  
Job time: 30 secs

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: April 15, 2003, 08:56:35 ; Search time 20 Seconds  
(without alignments)  
1051.540 Million cell updates/sec

Title: US-09-831-061-2

Perfect score: 344

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Searched: 248812 seqs, 61136040 residues

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Minimum DB seq length: 0

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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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5	8	2.3	66	9	US-09-922-199A-14
6	8	2.3	191	9	US-09-738-626-3880
7	8	2.3	269	10	US-09-965-703-54
8	8	2.3	283	12	US-10-042-417-50
9	8	2.3	332	9	US-09-764-868-1040
10	8	2.3	516	9	US-09-291-417-6
11	8	2.3	547	10	US-09-771-161A-272
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13	8	2.3	670	9	US-09-298-523B-63
14	8	2.3	701	9	US-09-298-523B-62
15	8	2.3	707	9	US-09-298-523B-3
16	8	2.3	711	9	US-09-298-523B-3
17	8	2.3	891	9	US-09-976-059-18
18	7	2.0	95	9	US-09-834-794A-21
19	7	2.0	95	10	US-09-834-795A-21
20	7	2.0	96	9	US-10-164-621-2
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23	7	2.0	96	10	US-09-988-598-2606
24	7	2.0	111	10	US-09-864-761-39500
25	7	2.0	113	10	US-09-864-761-39507
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28	7	2.0	132	12	US-10-078-929-22
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95	6	1.7	132	9	US-09-981-876-147	Sequence 147, App	168	6	1.7	315	10	US-09-983-306-3	Sequence 3, Appl
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99	6	1.7	133	10	US-09-908-711-90	Sequence 90, Appl	172	6	1.7	318	10	US-09-815-242-5784	Sequence 5784, App
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101	6	1.7	140	10	US-09-764-887-289	Sequence 289, App	174	6	1.7	321	9	US-09-738-626-486	Sequence 186, App
102	6	1.7	143	8	US-08-981-087A-4	Sequence 4, Appl	175	6	1.7	321	9	US-10-051-643-182	Sequence 182, App
103	6	1.7	147	10	US-09-823-038A-35	Sequence 35, Appl	176	6	1.7	331	9	US-09-880-505-182	Sequence 182, App
104	6	1.7	152	10	US-09-777-558-6	Sequence 6, Appl	177	6	1.7	331	9	US-09-738-626-4771	Sequence 4771, App
105	6	1.7	162	10	US-09-800-528-2	Sequence 2, Appl	178	6	1.7	335	10	US-09-968-851-44	Sequence 44, Appl
106	6	1.7	164	10	US-09-925-300-1451	Sequence 1451, App	179	6	1.7	335	10	US-09-815-242-12780	Sequence 12780, A
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108	6	1.7	170	10	US-09-818-066-49	Sequence 49, Appl	181	6	1.7	337	9	US-10-063-547-74	Sequence 74, Appl
109	6	1.7	172	10	US-09-777-558-14	Sequence 14, Appl	182	6	1.7	337	9	US-09-738-626-3997	Sequence 3997, App
110	6	1.7	173	10	US-09-800-528-13	Sequence 13, Appl	183	6	1.7	337	9	US-10-174-590-268	Sequence 268, App
111	6	1.7	173	10	US-09-815-242-12386	Sequence 12386, A	184	6	1.7	337	9	US-10-176-758-268	Sequence 268, App
112	6	1.7	173	10	US-09-815-242-12822	Sequence 12822, A	185	6	1.7	337	9	US-10-063-616-74	Sequence 74, Appl
113	6	1.7	173	10	US-09-815-242-13135	Sequence 13135, A	186	6	1.7	337	9	US-10-175-737-268	Sequence 268, App
114	6	1.7	174	10	US-09-818-066-42	Sequence 42, Appl	187	6	1.7	337	9	US-10-063-502-74	Sequence 74, Appl
115	6	1.7	174	10	US-09-818-066-43	Sequence 43, Appl	188	6	1.7	337	9	US-10-173-706-268	Sequence 268, App
116	6	1.7	174	10	US-09-818-066-45	Sequence 45, Appl	189	6	1.7	337	9	US-10-173-738-268	Sequence 268, App
117	6	1.7	174	10	US-09-818-066-46	Sequence 46, Appl	190	6	1.7	337	9	US-10-173-752-268	Sequence 268, App
118	6	1.7	174	10	US-09-818-066-47	Sequence 47, Appl	191	6	1.7	337	9	US-10-176-482-268	Sequence 268, App
119	6	1.7	174	10	US-09-818-066-48	Sequence 48, Appl	192	6	1.7	337	9	US-10-176-482-268	Sequence 268, App
120	6	1.7	174	10	US-09-818-066-50	Sequence 50, Appl	193	6	1.7	337	9	US-10-176-913-268	Sequence 268, App
121	6	1.7	174	10	US-09-818-066-51	Sequence 51, Appl	194	6	1.7	337	9	US-10-176-913-268	Sequence 268, App
122	6	1.7	174	10	US-09-818-066-52	Sequence 52, Appl	195	6	1.7	337	9	US-10-180-552-268	Sequence 268, App
123	6	1.7	174	10	US-09-818-066-53	Sequence 53, Appl	196	6	1.7	337	9	US-10-180-557-268	Sequence 268, App
124	6	1.7	174	10	US-09-818-066-54	Sequence 54, Appl	197	6	1.7	337	9	US-10-173-700-268	Sequence 268, App
125	6	1.7	174	10	US-09-818-066-55	Sequence 55, Appl	198	6	1.7	337	9	US-10-174-572-268	Sequence 268, App
126	6	1.7	174	10	US-09-818-066-56	Sequence 56, Appl	199	6	1.7	337	9	US-10-174-579-268	Sequence 268, App
127	6	1.7	174	10	US-09-818-066-57	Sequence 57, Appl	200	6	1.7	337	9	US-10-174-582-268	Sequence 268, App
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134	6	1.7	208	9	US-09-738-626-6854	Sequence 6854, App	207	6	1.7	337	9	US-10-176-750-268	Sequence 268, App
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136	6	1.7	219	10	US-09-974-449-38	Sequence 38, Appl	209	6	1.7	337	9	US-10-176-987-268	Sequence 268, App
137	6	1.7	223	10	US-09-970-711-11	Sequence 11, Appl	210	6	1.7	337	9	US-10-176-991-268	Sequence 268, App
138	6	1.7	224	9	US-10-001-254-57	Sequence 57, Appl	211	6	1.7	337	9	US-10-176-992-268	Sequence 268, App
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141	6	1.7	234	10	US-09-839-980-517	Sequence 517, App	214	6	1.7	337	9	US-10-173-695-268	Sequence 268, App
142	6	1.7	240	9	US-09-880-748-1918	Sequence 1918, App	215	6	1.7	337	9	US-10-173-697-268	Sequence 268, App
143	6	1.7	240	10	US-09-815-242-13469	Sequence 13469, A	216	6	1.7	337	9	US-10-173-705-268	Sequence 268, App
144	6	1.7	241	10	US-09-819-917-5	Sequence 5, Appl	217	6	1.7	337	9	US-10-174-585-268	Sequence 268, App
145	6	1.7	246	9	US-09-738-626-5858	Sequence 5858, App	218	6	1.7	337	9	US-10-174-585-268	Sequence 268, App
146	6	1.7	253	9	US-09-968-851-30	Sequence 30, Appl	219	6	1.7	337	9	US-10-174-586-268	Sequence 268, App
147	6	1.7	253	9	US-09-738-626-4362	Sequence 4362, App	220	6	1.7	337	9	US-10-173-747-268	Sequence 268, App
148	6	1.7	257	9	US-09-924-900-6	Sequence 6, Appl	221	6	1.7	337	9	US-10-176-925-268	Sequence 268, App
149	6	1.7	262	9	US-09-764-868-644	Sequence 644, App	222	6	1.7	337	9	US-10-176-978-268	Sequence 268, App
150	6	1.7	264	9	US-10-043-487-254	Sequence 254, App	223	6	1.7	337	9	US-10-179-510-268	Sequence 268, App
151	6	1.7	267	9	US-09-981-353-82	Sequence 82, Appl	224	6	1.7	337	9	US-10-180-543-268	Sequence 268, App
152	6	1.7	269	10	US-09-777-558-17	Sequence 17, Appl	225	6	1.7	337	9	US-10-180-544-268	Sequence 268, App
153	6	1.7	270	9	US-09-968-851-32	Sequence 32, Appl	226	6	1.7	337	9	US-10-180-546-268	Sequence 268, App
154	6	1.7	270	10	US-09-925-301-1205	Sequence 1205, App	227	6	1.7	337	9	US-10-180-547-268	Sequence 268, App
155	6	1.7	273	9	US-09-738-626-4392	Sequence 4392, App	228	6	1.7	337	9	US-10-176-925-268	Sequence 268, App
156	6	1.7	273	10	US-09-900-575-40	Sequence 40, Appl	229	6	1.7	337	9	US-10-176-978-268	Sequence 268, App
157	6	1.7	280	10	US-09-983-306-1	Sequence 1, Appl	230	6	1.7	337	9	US-10-179-510-268	Sequence 268, App
158	6	1.7	283	9	US-09-738-626-3533	Sequence 3533, App	231	6	1.7	337	9	US-10-180-543-268	Sequence 268, App
159	6	1.7	293	9	US-09-946-406-6	Sequence 6, Appl	232	6	1.7	337	9	US-10-180-544-268	Sequence 268, App
160	6	1.7	294	9	US-09-877-650-11	Sequence 11, Appl	233	6	1.7	337	9	US-10-180-546-268	Sequence 268, App
161	6	1.7	294	10	US-09-871-856-11	Sequence 11, Appl	234	6	1.7	337	9	US-10-180-547-268	Sequence 268, App
162	6	1.7	295	9	US-10-106-534-4	Sequence 4, Appl	235	6	1.7	337	9	US-10-180-549-268	Sequence 268, App
163	6	1.7	297	10	US-09-925-297-635	Sequence 635, App	236	6	1.7	337	9	US-10-180-555-268	Sequence 268, App
164	6	1.7	299	10	US-09-739-254-73	Sequence 73, Appl	237	6	1.7	337	9	US-10-180-559-268	Sequence 268, App
165	6	1.7	299	10	US-09-904-615-73	Sequence 73, Appl	238	6	1.7	337	9	US-10-181-000-268	Sequence 268, App





385	6	1.7	337	9	US-10-201-534-268	Sequence 268, App	458	6	1.7	350	9	US-09-906-838-236	Sequence 236, App
386	6	1.7	337	9	US-10-201-770-268	Sequence 268, App	459	6	1.7	350	9	US-09-907-813-236	Sequence 236, App
387	6	1.7	337	9	US-10-201-855-268	Sequence 268, App	460	6	1.7	350	9	US-09-907-942-236	Sequence 236, App
388	6	1.7	337	9	US-10-201-855-268	Sequence 268, App	461	6	1.7	350	9	US-09-904-820-236	Sequence 236, App
389	6	1.7	337	9	US-10-202-469-268	Sequence 268, App	462	6	1.7	350	9	US-09-904-859-236	Sequence 236, App
390	6	1.7	337	9	US-10-202-470-268	Sequence 268, App	463	6	1.7	350	9	US-09-909-204-236	Sequence 236, App
391	6	1.7	337	9	US-10-202-476-268	Sequence 268, App	464	6	1.7	350	9	US-09-904-786-236	Sequence 236, App
392	6	1.7	337	9	US-10-202-934-268	Sequence 268, App	465	6	1.7	350	9	US-09-906-646-236	Sequence 236, App
393	6	1.7	337	9	US-10-202-935-268	Sequence 268, App	466	6	1.7	350	9	US-09-906-700-236	Sequence 236, App
394	6	1.7	337	9	US-10-202-936-268	Sequence 268, App	467	6	1.7	350	9	US-09-902-903-236	Sequence 236, App
395	6	1.7	337	9	US-10-202-939-268	Sequence 268, App	468	6	1.7	350	9	US-09-903-749A-236	Sequence 236, App
396	6	1.7	337	9	US-10-205-504-268	Sequence 268, App	469	6	1.7	350	9	US-09-903-786-236	Sequence 236, App
397	6	1.7	337	9	US-10-205-509-268	Sequence 268, App	470	6	1.7	350	9	US-09-902-736-236	Sequence 236, App
398	6	1.7	337	9	US-10-205-895-268	Sequence 268, App	471	6	1.7	350	9	US-09-904-119-236	Sequence 236, App
399	6	1.7	337	9	US-10-205-895-268	Sequence 268, App	472	6	1.7	350	9	US-09-904-956-236	Sequence 236, App
400	6	1.7	337	9	US-10-205-899-268	Sequence 268, App	473	6	1.7	350	9	US-09-907-794-236	Sequence 236, App
401	6	1.7	337	9	US-10-205-909-268	Sequence 268, App	474	6	1.7	350	9	US-10-063-518-8	Sequence 8, Appl
402	6	1.7	337	9	US-10-227-693-74	Sequence 74, Appl	475	6	1.7	350	9	US-10-063-598-8	Sequence 8, Appl
403	6	1.7	337	9	US-10-006-818A-423	Sequence 423, App	476	6	1.7	350	9	US-10-227-693-8	Sequence 8, Appl
404	6	1.7	337	9	US-10-183-002-268	Sequence 268, App	477	6	1.7	350	9	US-09-902-692-236	Sequence 236, App
405	6	1.7	337	9	US-10-184-621-268	Sequence 268, App	478	6	1.7	350	9	US-09-903-520-236	Sequence 236, App
406	6	1.7	337	9	US-10-184-638-268	Sequence 268, App	479	6	1.7	350	9	US-09-903-943-236	Sequence 236, App
407	6	1.7	337	9	US-10-187-752-268	Sequence 268, App	480	6	1.7	350	9	US-09-904-462-236	Sequence 236, App
408	6	1.7	337	9	US-10-187-887-268	Sequence 268, App	481	6	1.7	350	9	US-09-905-056-236	Sequence 236, App
409	6	1.7	337	9	US-10-194-461-268	Sequence 268, App	482	6	1.7	350	9	US-09-907-925-236	Sequence 236, App
410	6	1.7	337	9	US-10-195-892-268	Sequence 268, App	483	6	1.7	350	9	US-09-904-553-236	Sequence 236, App
411	6	1.7	337	9	US-10-195-892-268	Sequence 268, App	484	6	1.7	350	9	US-09-905-381-236	Sequence 236, App
412	6	1.7	337	9	US-10-196-751-268	Sequence 268, App	485	6	1.7	350	9	US-09-909-064-236	Sequence 236, App
413	6	1.7	337	9	US-10-197-694-268	Sequence 268, App	486	6	1.7	350	10	US-09-909-320-236	Sequence 236, App
414	6	1.7	337	9	US-10-197-697-268	Sequence 268, App	487	6	1.7	350	10	US-09-909-088B-236	Sequence 236, App
415	6	1.7	337	9	US-10-197-707-268	Sequence 268, App	488	6	1.7	350	12	US-10-006-867-8	Sequence 8, Appl
416	6	1.7	337	9	US-10-199-303-268	Sequence 268, App	489	6	1.7	351	10	US-09-923-301-1426	Sequence 1426, Ap
417	6	1.7	337	9	US-10-199-318-268	Sequence 268, App	490	6	1.7	353	9	US-09-968-851-40	Sequence 40, Appl
418	6	1.7	337	9	US-10-199-458-268	Sequence 268, App	491	6	1.7	353	9	US-09-738-626-3982	Sequence 3982, Ap
419	6	1.7	337	9	US-10-199-462-268	Sequence 268, App	492	6	1.7	358	9	US-09-893-519A-13	Sequence 13, Appl
420	6	1.7	337	9	US-10-201-324-268	Sequence 268, App	493	6	1.7	360	10	US-09-815-242-12094	Sequence 12094, A
421	6	1.7	337	9	US-10-201-328-268	Sequence 268, App	494	6	1.7	363	10	US-09-968-851-26	Sequence 26, Appl
422	6	1.7	337	9	US-10-201-527-268	Sequence 268, App	495	6	1.7	365	10	US-09-815-242-11972	Sequence 11972, A
423	6	1.7	337	9	US-10-201-529-268	Sequence 268, App	496	6	1.7	373	10	US-09-789-386-6	Sequence 6, Appl
424	6	1.7	337	9	US-10-205-502-268	Sequence 268, App	497	6	1.7	373	10	US-08-785-205-6	Sequence 6, Appl
425	6	1.7	337	9	US-10-205-511-268	Sequence 268, App	498	6	1.7	373	10	US-09-893-348-24	Sequence 24, Appl
426	6	1.7	337	9	US-10-205-902-268	Sequence 268, App	499	6	1.7	373	12	US-10-109-860-2	Sequence 2, Appl
427	6	1.7	337	9	US-10-202-409-268	Sequence 268, App	500	6	1.7	374	9	US-09-968-851-28	Sequence 28, Appl
428	6	1.7	337	9	US-10-202-411-268	Sequence 268, App	501	6	1.7	374	9	US-09-934-900-19	Sequence 19, Appl
429	6	1.7	337	9	US-10-202-472-268	Sequence 268, App	502	6	1.7	380	9	US-09-934-900-12	Sequence 12, Appl
430	6	1.7	337	9	US-10-205-502-268	Sequence 268, App	503	6	1.7	381	9	US-09-808-602-6	Sequence 6, Appl
431	6	1.7	337	9	US-10-205-507-268	Sequence 268, App	504	6	1.7	381	9	US-09-968-851-36	Sequence 36, Appl
432	6	1.7	337	9	US-10-205-511-268	Sequence 268, App	505	6	1.7	381	9	US-09-977-418-22	Sequence 22, Appl
433	6	1.7	337	9	US-10-205-907-268	Sequence 268, App	506	6	1.7	381	9	US-09-934-900-16	Sequence 16, Appl
434	6	1.7	337	9	US-10-194-456-268	Sequence 268, App	507	6	1.7	383	9	US-09-908-504A-1	Sequence 1, Appl
435	6	1.7	337	9	US-10-196-758-268	Sequence 268, App	508	6	1.7	383	10	US-09-771-956-27	Sequence 27, Appl
436	6	1.7	337	9	US-10-198-770-268	Sequence 268, App	509	6	1.7	383	10	US-09-912-020-265	Sequence 265, App
437	6	1.7	337	9	US-10-199-308-268	Sequence 268, App	510	6	1.7	383	10	US-09-815-242-10033	Sequence 10033, A
438	6	1.7	337	9	US-10-200-617-268	Sequence 268, App	511	6	1.7	384	9	US-09-934-900-17	Sequence 17, Appl
439	6	1.7	337	9	US-10-205-893-268	Sequence 268, App	512	6	1.7	388	10	US-09-925-300-1618	Sequence 1618, Ap
440	6	1.7	337	9	US-10-205-893-268	Sequence 268, App	513	6	1.7	389	9	US-09-821-877-2	Sequence 2, Appl
441	6	1.7	337	10	US-09-946-143-2	Sequence 2, Appl	514	6	1.7	390	10	US-09-815-242-5770	Sequence 5770, Ap
442	6	1.7	337	12	US-10-006-867-74	Sequence 74, Appl	515	6	1.7	392	10	US-09-815-242-12723	Sequence 12723, A
443	6	1.7	337	12	US-10-052-586-268	Sequence 268, App	516	6	1.7	393	9	US-09-025-327-4	Sequence 4, Appl
444	6	1.7	340	9	US-10-013-477-14	Sequence 14, Appl	517	6	1.7	393	10	US-09-776-695-32	Sequence 32, Appl
445	6	1.7	341	10	US-09-771-956-26	Sequence 26, Appl	518	6	1.7	393	10	US-09-732-384-3	Sequence 3, Appl
446	6	1.7	342	9	US-10-001-857-201	Sequence 201, App	519	6	1.7	393	10	US-09-860-211-9	Sequence 9, Appl
447	6	1.7	350	9	US-09-905-291A-236	Sequence 236, App	520	6	1.7	394	12	US-10-155-059-4	Sequence 4, Appl
448	6	1.7	350	9	US-09-976-736-9	Sequence 9, Appl	521	6	1.7	396	9	US-09-934-900-18	Sequence 18, Appl
449	6	1.7	350	9	US-10-063-534-268	Sequence 8, Appl	522	6	1.7	396	9	US-09-934-900-22	Sequence 22, Appl
450	6	1.7	350	9	US-09-902-853-236	Sequence 236, App	523	6	1.7	398	9	US-09-738-626-6516	Sequence 6516, Ap
451	6	1.7	350	9	US-09-907-824-236	Sequence 236, App	524	6	1.7	398	9	US-10-081-816-19	Sequence 19, Appl
452	6	1.7	350	9	US-09-907-841-236	Sequence 236, App	525	6	1.7	398	9	US-09-934-900-20	Sequence 20, Appl
453	6	1.7	350	9	US-09-904-011-236	Sequence 236, App	526	6	1.7	398	10	US-09-912-020-304	Sequence 304, App
454	6	1.7	350	9	US-10-201-310-2	Sequence 2, Appl	527	6	1.7	398	10	US-09-731-872-288	Sequence 288, App
455	6	1.7	350	9	US-10-063-616-8	Sequence 8, Appl	528	6	1.7	399	9	US-09-764-968-850	Sequence 850, App
456	6	1.7	350	9	US-09-906-742-236	Sequence 236, App	529	6	1.7	401	9	US-09-968-851-34	Sequence 34, Appl
457	6	1.7	350	9	US-10-063-502-8	Sequence 8, Appl	530	6	1.7	401	9	US-09-738-626-3705	Sequence 3705, Ap

531	6	1.7	401	9	US-09-738-626-5923	Sequence 5923, Ap	604	597	9	US-09-997-182-129	Sequence 129, App
532	6	1.7	401	9	US-09-738-626-6636	Sequence 6636, Ap	605	600	9	US-10-003-392-20	Sequence 20, Appl
533	6	1.7	402	10	US-09-854-731-16	Sequence 16, Appl	606	605	9	US-10-128-870-24	Sequence 24, Appl
534	6	1.7	403	10	US-09-731-872-249	Sequence 249, App	607	605	9	US-10-131-685-24	Sequence 24, Appl
535	6	1.7	403	9	US-09-934-900-2	Sequence 2, Appl	608	615	9	US-09-908-193-26	Sequence 26, Appl
536	6	1.7	408	9	US-10-102-806-639	Sequence 639, Appl	609	615	9	US-09-908-193-27	Sequence 27, Appl
537	6	1.7	408	12	US-10-109-860-4	Sequence 4, Appl	610	615	9	US-09-882-774-1	Sequence 1, Appl
538	6	1.7	410	10	US-09-866-562-41	Sequence 41, Appl	611	641	10	US-10-267-311-51	Sequence 51, Appl
539	6	1.7	410	10	US-09-815-242-10639	Sequence 10639, A	612	641	10	US-09-876-527-2	Sequence 2, Appl
540	6	1.7	411	10	US-09-815-242-4909	Sequence 4909, Ap	613	644	10	US-10-223-441-2	Sequence 2, Appl
541	6	1.7	412	12	US-10-090-624-1	Sequence 12, Appl	614	644	10	US-09-943-692-2	Sequence 2, Appl
542	6	1.7	413	10	US-09-919-703-12	Sequence 11301, A	615	654	12	US-10-080-624-16	Sequence 16, Appl
543	6	1.7	416	10	US-09-815-242-11301	Sequence 11301, A	616	672	9	US-09-928-530-5	Sequence 5, Appl
544	6	1.7	416	10	US-09-881-752A-172	Sequence 172, App	617	672	9	US-10-162-012-30	Sequence 30, Appl
545	6	1.7	421	10	US-09-815-242-11192	Sequence 11192, A	618	674	9	US-10-028-072-36	Sequence 36, Appl
546	6	1.7	423	10	US-09-815-242-10566	Sequence 86, Appl	619	674	9	US-10-121-049-36	Sequence 36, Appl
547	6	1.7	425	9	US-09-738-626-4016	Sequence 4016, Ap	620	674	9	US-10-123-904-36	Sequence 36, Appl
548	6	1.7	427	9	US-09-764-868-894	Sequence 894, App	621	674	9	US-10-140-470-36	Sequence 36, Appl
549	6	1.7	428	9	US-09-906-514-4	Sequence 4, Appl	622	674	9	US-10-173-746-36	Sequence 36, Appl
550	6	1.7	429	9	US-09-738-626-5628	Sequence 5628, Ap	623	674	9	US-10-176-918-36	Sequence 36, Appl
551	6	1.7	431	8	US-08-981-087A-1	Sequence 1, Appl	624	674	9	US-10-176-921-36	Sequence 36, Appl
552	6	1.7	432	9	US-09-910-186A-16	Sequence 16, Appl	625	674	9	US-10-137-865-36	Sequence 36, Appl
553	6	1.7	432	9	US-09-910-186A-34	Sequence 34, Appl	626	674	9	US-10-140-474-36	Sequence 36, Appl
554	6	1.7	432	10	US-09-815-242-10566	Sequence 10566, A	627	674	9	US-10-142-431-36	Sequence 36, Appl
555	6	1.7	433	9	US-09-906-514-2	Sequence 2, Appl	628	674	9	US-10-143-114-36	Sequence 36, Appl
556	6	1.7	442	9	US-09-738-626-5860	Sequence 5860, Ap	629	674	9	US-10-140-002-36	Sequence 36, Appl
557	6	1.7	446	9	US-09-866-570A-74	Sequence 74, Appl	630	674	9	US-10-142-419-36	Sequence 36, Appl
558	6	1.7	446	10	US-09-866-572A-74	Sequence 74, Appl	631	674	9	US-10-142-419-36	Sequence 36, Appl
559	6	1.7	448	10	US-08-871-212-8	Sequence 8, Appl	632	674	9	US-10-123-262-36	Sequence 36, Appl
560	6	1.7	456	10	US-09-323-998D-20	Sequence 20, Appl	633	674	9	US-10-142-419-36	Sequence 36, Appl
561	6	1.7	461	12	US-10-013-823-3	Sequence 3, Appl	634	674	9	US-10-142-419-36	Sequence 36, Appl
562	6	1.7	462	10	US-09-745-763-189	Sequence 189, App	635	674	9	US-10-141-755-36	Sequence 36, Appl
563	6	1.7	471	9	US-10-003-392-10	Sequence 10, Appl	636	674	9	US-10-143-032-36	Sequence 36, Appl
564	6	1.7	477	9	US-09-738-626-6985	Sequence 6985, Ap	637	689	9	US-09-738-626-3675	Sequence 3675, Ap
565	6	1.7	478	9	US-09-924-340-108	Sequence 108, App	638	690	9	US-09-298-523B-61	Sequence 61, Appl
566	6	1.7	478	9	US-09-992-600A-108	Sequence 108, App	639	691	8	US-08-834-666A-12	Sequence 12, Appl
567	6	1.7	478	9	US-09-746-783-184	Sequence 184, App	640	691	8	US-08-834-666A-22	Sequence 22, Appl
568	6	1.7	484	9	US-10-212-933-4	Sequence 4, Appl	641	716	10	US-09-298-523B-1	Sequence 1, Appl
569	6	1.7	486	10	US-09-793-848A-4	Sequence 4, Appl	642	716	10	US-09-815-242-12403	Sequence 12403, A
570	6	1.7	487	9	US-10-023-437-19	Sequence 19, Appl	643	722	10	US-09-815-242-11000	Sequence 11000, A
571	6	1.7	488	10	US-09-801-196-26	Sequence 26, Appl	644	730	9	US-09-298-523B-68	Sequence 68, Appl
572	6	1.7	495	9	US-10-003-392-8	Sequence 8, Appl	645	731	10	US-09-910-174A-15	Sequence 15, Appl
573	6	1.7	497	10	US-09-896-896A-1	Sequence 1, Appl	646	751	9	US-09-738-626-6525	Sequence 6525, Ap
574	6	1.7	497	10	US-09-753-126-1	Sequence 1, Appl	647	775	9	US-09-738-626-3773	Sequence 3773, Ap
575	6	1.7	498	10	US-09-323-998D-57	Sequence 57, Appl	648	782	10	US-09-866-582-16	Sequence 16, Appl
576	6	1.7	500	10	US-10-157-855-17	Sequence 17, Appl	649	783	10	US-09-864-761-38209	Sequence 38209, A
577	6	1.7	500	10	US-09-323-998D-58	Sequence 58, Appl	650	802	10	US-09-757-049A-1	Sequence 1, Appl
578	6	1.7	500	10	US-09-323-998D-59	Sequence 59, Appl	651	803	10	US-09-738-363-12	Sequence 12, Appl
579	6	1.7	502	10	US-09-323-998D-56	Sequence 56, Appl	652	803	10	US-09-801-368-394	Sequence 394, App
580	6	1.7	504	10	US-09-765-205-40	Sequence 40, Appl	653	807	10	US-09-742-312-2	Sequence 2, Appl
581	6	1.7	506	9	US-10-108-605-295	Sequence 295, App	654	809	9	US-10-078-770-124	Sequence 124, App
582	6	1.7	507	10	US-09-876-187-2	Sequence 2, Appl	655	811	9	US-09-975-719-93	Sequence 93, Appl
583	6	1.7	507	10	US-09-749-728B-13	Sequence 13, Appl	656	852	9	US-09-738-626-6999	Sequence 6999, App
584	6	1.7	522	10	US-09-815-242-11002	Sequence 11002, A	657	862	10	US-09-742-312-4	Sequence 4, Appl
585	6	1.7	522	12	US-10-090-624-4	Sequence 4, Appl	658	873	1	US-08-911-824-61	Sequence 61, Appl
586	6	1.7	523	9	US-10-102-806-721	Sequence 721, App	659	915	10	US-09-817-514A-6	Sequence 6, Appl
587	6	1.7	527	9	US-09-935-642-13	Sequence 13, Appl	660	916	9	US-09-738-626-6353	Sequence 6353, Ap
588	6	1.7	531	10	US-09-833-790-255	Sequence 255, App	661	923	9	US-09-820-843A-112	Sequence 112, App
589	6	1.7	533	10	US-09-815-242-11376	Sequence 11376, A	662	923	9	US-09-298-523B-60	Sequence 60, Appl
590	6	1.7	535	9	US-09-968-851-38	Sequence 38, Appl	663	1012	10	US-09-876-527-16	Sequence 16, Appl
591	6	1.7	551	10	US-09-815-242-10500	Sequence 10500, A	664	1026	9	US-09-947-063-4	Sequence 4, Appl
592	6	1.7	552	10	US-09-824-735-4	Sequence 4, Appl	665	1026	9	US-09-947-063-11	Sequence 11, Appl
593	6	1.7	563	10	US-09-793-848A-2	Sequence 2, Appl	666	1036	9	US-09-947-063-12	Sequence 12, Appl
594	6	1.7	563	10	US-09-815-242-13430	Sequence 13430, A	667	1084	12	US-10-071-900-3	Sequence 3, Appl
595	6	1.7	565	9	US-10-081-051-35	Sequence 35, Appl	668	1184	9	US-09-978-295A-425	Sequence 425, App
596	6	1.7	568	9	US-09-738-626-4343	Sequence 4343, Ap	669	1184	9	US-09-978-697-425	Sequence 425, App
597	6	1.7	568	9	US-09-896-738-118	Sequence 118, App	670	1184	9	US-09-978-192A-425	Sequence 425, App
598	6	1.7	584	10	US-09-896-738-118	Sequence 118, App	671	1184	9	US-09-999-832A-425	Sequence 425, App
599	6	1.7	584	10	US-09-810-174A-16	Sequence 16, Appl	672	1184	9	US-09-978-189-425	Sequence 425, App
600	6	1.7	584	10	US-09-955-866-12	Sequence 12, Appl	673	1184	9	US-10-028-072-394	Sequence 394, App
601	6	1.7	592	10	US-09-753-126-4	Sequence 4, Appl	674	1184	9	US-10-121-049-394	Sequence 394, App
602	6	1.7	597	9	US-09-996-634-129	Sequence 129, App	675	1184	9	US-10-123-904-394	Sequence 394, App
603	6	1.7	597	9	US-09-997-181-129	Sequence 129, App	676	1184	9	US-10-140-470-394	Sequence 394, App

677	1.7	1184	9	US-10-175-746-394	Sequence 394, App	750	6	1.7	2697	10	US-09-961-527A-5	Sequence 5, Appl1
678	1.7	1184	9	US-10-176-918-394	Sequence 394, App	751	6	1.7	2724	9	US-09-808-602-13	Sequence 13, Appl
679	1.7	1184	9	US-10-178-921-394	Sequence 394, App	752	6	1.7	2733	9	US-09-808-602-8	Sequence 8, Appl1
680	1.7	1184	9	US-10-137-865-394	Sequence 394, App	753	6	1.7	2764	9	US-09-808-602-80	Sequence 80, Appl
681	1.7	1184	9	US-10-140-474-394	Sequence 394, App	754	6	1.7	2765	9	US-09-808-602-84	Sequence 84, Appl
682	1.7	1184	9	US-10-142-431-394	Sequence 394, App	755	6	1.7	2802	9	US-09-808-602-81	Sequence 81, Appl
683	1.7	1184	9	US-10-143-114-394	Sequence 394, App	756	6	1.7	3158	10	US-09-815-242-12611	Sequence 12611, A
684	1.7	1184	9	US-10-140-002-394	Sequence 394, App	757	6	1.7	6281	10	US-09-815-242-12996	Sequence 12996, A
685	1.7	1184	9	US-09-978-608A-425	Sequence 425, App	758	6	1.7	26926	9	US-09-759-508B-2	Sequence 2, Appl1
686	1.7	1184	9	US-10-142-419-394	Sequence 394, App	759	5	1.5	6	10	US-09-835-087-19	Sequence 19, Appl
687	1.7	1184	9	US-09-978-191A-425	Sequence 425, App	760	5	1.5	8	9	US-09-770-595A-9	Sequence 9, Appl1
688	1.7	1184	9	US-09-978-403A-425	Sequence 425, App	761	5	1.5	8	10	US-09-844-988-21	Sequence 21, Appl
689	1.7	1184	9	US-09-978-564A-425	Sequence 425, App	762	5	1.5	8	10	US-09-844-908-21	Sequence 21, Appl
690	1.7	1184	9	US-09-978-585A-425	Sequence 425, App	763	5	1.5	9	10	US-09-779-308-191	Sequence 191, App
691	1.7	1184	9	US-10-017-081A-425	Sequence 425, App	764	5	1.5	10	9	US-09-017-743C-87	Sequence 87, Appl
692	1.7	1184	9	US-10-123-282-394	Sequence 394, App	765	5	1.5	10	9	US-09-955-732-16	Sequence 16, Appl
693	1.7	1184	9	US-10-142-423-394	Sequence 394, App	766	5	1.5	10	9	US-09-945-917-18	Sequence 18, Appl
694	1.7	1184	9	US-09-978-824-425	Sequence 425, App	767	5	1.5	10	10	US-09-955-732-16	Sequence 4, Appl1
695	1.7	1184	9	US-09-981-915A-425	Sequence 425, App	768	5	1.5	10	10	US-09-770-595A-4	Sequence 4, Appl1
696	1.7	1184	9	US-09-999-833A-425	Sequence 425, App	769	5	1.5	10	10	US-09-779-308-230	Sequence 230, App
697	1.7	1184	9	US-10-121-050-394	Sequence 394, App	770	5	1.5	10	10	US-09-779-308-254	Sequence 254, App
698	1.7	1184	9	US-10-141-755-394	Sequence 394, App	771	5	1.5	10	10	US-09-779-308-444	Sequence 444, App
699	1.7	1184	9	US-10-167-749-425	Sequence 425, App	772	5	1.5	11	9	US-10-033-741-23	Sequence 23, Appl
700	1.7	1184	9	US-09-918-585A-425	Sequence 425, App	773	5	1.5	11	12	US-09-734-520-84	Sequence 84, Appl
701	1.7	1184	9	US-10-143-032-394	Sequence 394, App	774	5	1.5	11	12	US-10-012-034A-84	Sequence 84, Appl
702	1.7	1187	10	US-09-768-436-4	Sequence 4, Appl1	775	5	1.5	12	10	US-09-839-666-8	Sequence 8, Appl1
703	1.7	1192	10	US-09-789-386-2	Sequence 2, Appl1	776	5	1.5	12	10	US-09-839-666-9	Sequence 9, Appl1
704	1.7	1192	10	US-09-758-140-6	Sequence 6, Appl1	777	5	1.5	12	10	US-09-770-595A-7	Sequence 7, Appl1
705	1.7	1192	10	US-09-833-348-23	Sequence 23, Appl	778	5	1.5	12	10	US-09-832-723-19	Sequence 19, Appl
706	1.7	1192	10	US-09-972-599A-6	Sequence 6, Appl1	779	5	1.5	13	9	US-09-968-436B-9	Sequence 9, Appl1
707	1.7	1196	9	US-09-823-394-2	Sequence 2, Appl1	780	5	1.5	13	9	US-10-044-703-34	Sequence 34, Appl
708	1.7	1214	9	US-09-945-901-54	Sequence 54, Appl	781	5	1.5	13	9	US-10-033-741-62	Sequence 62, Appl
709	1.7	1214	9	US-10-007-747-54	Sequence 54, Appl	782	5	1.5	13	10	US-09-879-936-25	Sequence 25, Appl
710	1.7	1214	9	US-10-038-937-54	Sequence 54, Appl	783	5	1.5	14	9	US-09-813-333-34	Sequence 34, Appl
711	1.7	1215	10	US-09-815-242-5908	Sequence 5908, Ap	784	5	1.5	14	9	US-10-024-123-40	Sequence 40, Appl
712	1.7	1219	9	US-09-945-901-50	Sequence 50, Appl	785	5	1.5	14	10	US-09-903-412-9	Sequence 9, Appl1
713	1.7	1219	9	US-10-007-747-50	Sequence 50, Appl	786	5	1.5	15	9	US-10-211-069-9	Sequence 9, Appl1
714	1.7	1219	9	US-10-038-937-50	Sequence 50, Appl	787	5	1.5	15	10	US-09-916-201-7	Sequence 7, Appl1
715	1.7	1231	9	US-09-945-901-48	Sequence 48, Appl	788	5	1.5	16	9	US-09-967-237-16	Sequence 16, Appl
716	1.7	1231	9	US-10-007-747-48	Sequence 48, Appl	789	5	1.5	16	10	US-09-772-719-16	Sequence 16, Appl
717	1.7	1231	9	US-10-038-937-48	Sequence 48, Appl	790	5	1.5	17	9	US-09-984-245-308	Sequence 308, App
718	1.7	1236	9	US-09-945-901-6	Sequence 6, Appl1	791	5	1.5	17	9	US-09-966-262-308	Sequence 308, App
719	1.7	1236	9	US-10-007-747-6	Sequence 6, Appl1	792	5	1.5	17	9	US-09-880-748-2862	Sequence 2862, Ap
720	1.7	1236	9	US-10-038-937-6	Sequence 6, Appl1	793	5	1.5	17	9	US-09-983-966-308	Sequence 308, App
721	1.7	1239	9	US-09-945-901-52	Sequence 52, Appl	794	5	1.5	17	9	US-09-879-936-9	Sequence 9, Appl1
722	1.7	1239	9	US-10-007-747-52	Sequence 52, Appl	795	5	1.5	17	10	US-09-864-761-34508	Sequence 34508, A
723	1.7	1239	9	US-10-038-937-52	Sequence 52, Appl	796	5	1.5	17	10	US-09-880-713A-16	Sequence 16, Appl
724	1.7	1244	9	US-09-945-901-46	Sequence 46, Appl	797	5	1.5	17	10	US-09-988-842-7	Sequence 7, Appl1
725	1.7	1244	9	US-10-007-747-46	Sequence 46, Appl	798	5	1.5	17	10	US-09-864-761-40786	Sequence 40786, A
726	1.7	1244	9	US-10-038-937-46	Sequence 46, Appl	799	5	1.5	18	10	US-10-038-612-33	Sequence 33, Appl
727	1.7	1247	10	US-09-815-242-10145	Sequence 10145, A	800	5	1.5	19	9	US-10-038-612-34	Sequence 34, Appl
728	1.7	1269	10	US-09-815-242-13113	Sequence 13113, A	801	5	1.5	19	9	US-09-954-349-11	Sequence 11, Appl
729	1.7	1333	10	US-09-815-242-10936	Sequence 10936, A	802	5	1.5	20	9	US-10-038-612-151	Sequence 151, App
730	1.7	1354	10	US-09-808-571A-4	Sequence 4, Appl1	803	5	1.5	20	9	US-10-044-703-22	Sequence 22, Appl
731	1.7	1447	10	US-09-808-571A-4	Sequence 2, Appl1	804	5	1.5	20	10	US-09-864-761-34828	Sequence 34828, A
732	1.7	1460	10	US-09-815-242-13668	Sequence 13668, A	805	5	1.5	20	10	US-09-813-333-22	Sequence 22, Appl
733	1.7	1464	9	US-09-945-901-11	Sequence 11, Appl	806	5	1.5	21	9	US-10-124-800-15	Sequence 15, Appl
734	1.7	1464	9	US-10-007-747-11	Sequence 11, Appl	807	5	1.5	21	9	US-10-051-643-4	Sequence 4, Appl1
735	1.7	1464	9	US-10-038-937-11	Sequence 11, Appl	808	5	1.5	21	9	US-10-051-643-13	Sequence 13, Appl
736	1.7	1488	9	US-09-738-626-5495	Sequence 5495, Ap	809	5	1.5	21	9	US-09-880-505-4	Sequence 4, Appl1
737	1.7	1504	9	US-09-932-145-7	Sequence 7, Appl1	810	5	1.5	21	9	US-09-880-505-13	Sequence 13, Appl
738	1.7	1723	10	US-09-841-132-394	Sequence 394, App	811	5	1.5	21	10	US-09-775-923-17	Sequence 3, Appl1
739	1.7	1723	10	US-09-841-132-395	Sequence 395, App	812	5	1.5	22	9	US-09-349-755-9	Sequence 9, Appl1
740	1.7	1802	10	US-09-965-553-18	Sequence 18, Appl	813	5	1.5	22	9	US-09-349-755-16	Sequence 16, Appl
741	1.7	2008	9	US-09-736-968A-105	Sequence 105, App	814	5	1.5	22	9	US-09-349-755-35	Sequence 35, Appl
742	1.7	2008	10	US-09-736-969A-2	Sequence 2, Appl1	815	5	1.5	22	9	US-09-166-334-9	Sequence 9, Appl1
743	1.7	2008	10	US-09-736-969A-91	Sequence 91, Appl	816	5	1.5	22	9	US-09-166-334-16	Sequence 16, Appl
744	1.7	2008	10	US-09-736-960-88	Sequence 88, Appl	817	5	1.5	22	9	US-09-166-334-35	Sequence 35, Appl
745	1.7	2025	10	US-09-815-242-5703	Sequence 5703, Ap	818	5	1.5	22	9	US-09-955-732-18	Sequence 18, Appl
746	1.7	2026	10	US-09-801-368-86	Sequence 86, Appl	819	5	1.5	22	9	US-09-752-724-9	Sequence 9, Appl1
747	1.7	2120	9	US-10-051-311A-2	Sequence 2, Appl1	820	5	1.5	22	10	US-09-752-724-10	Sequence 10, Appl
748	1.7	2437	10	US-09-815-242-5834	Sequence 5834, Ap	821	5	1.5	22	10		
749	1.7	2472	10	US-09-815-242-5064	Sequence 5064, Ap	822	5	1.5	22	10		

823	5	1.5	22	10	US-09-864-761-44867	Sequence 44867, A	896	5	1.5	42	10	US-09-848-664-14	Sequence 14, Appl
824	5	1.5	22	10	US-09-985-297-46	Sequence 46, Appl	897	5	1.5	43	10	US-09-864-761-47609	Sequence 47609, A
825	5	1.5	22	10	US-09-350-206-9	Sequence 9, Appl	898	5	1.5	44	10	US-09-864-761-36103	Sequence 36103, A
826	5	1.5	22	10	US-09-350-206-16	Sequence 16, Appl	899	5	1.5	44	10	US-09-864-761-42196	Sequence 42196, A
827	5	1.5	22	10	US-09-350-206-35	Sequence 35, Appl	900	5	1.5	45	10	US-09-864-761-37820	Sequence 37820, A
828	5	1.5	22	10	US-09-925-442-31	Sequence 31, Appl	901	5	1.5	45	10	US-09-864-761-37820	Sequence 37820, A
829	5	1.5	22	10	US-09-912-425-3	Sequence 3, Appl	902	5	1.5	46	9	US-10-102-806-486	Sequence 1821, Ap
830	5	1.5	23	9	US-10-097-065-451	Sequence 451, App	903	5	1.5	46	9	US-10-102-806-486	Sequence 486, App
831	5	1.5	24	10	US-09-864-761-38685	Sequence 38685, A	904	5	1.5	47	9	US-09-864-761-44815	Sequence 44815, A
832	5	1.5	25	9	US-10-051-643-20	Sequence 20, Appl	905	5	1.5	47	9	US-09-812-485A-4	Sequence 4, Appl
833	5	1.5	25	9	US-09-880-505-20	Sequence 20, Appl	906	5	1.5	48	10	US-09-939-980-299	Sequence 299, App
834	5	1.5	25	9	US-09-967-237-53	Sequence 53, Appl	907	5	1.5	48	10	US-09-864-761-43341	Sequence 43341, A
835	5	1.5	25	9	US-10-044-708A-5	Sequence 5, Appl	908	5	1.5	49	10	US-09-764-860-391	Sequence 391, App
836	5	1.5	25	10	US-09-276-600-9	Sequence 9, Appl	909	5	1.5	50	9	US-10-032-896-585	Sequence 585, App
837	5	1.5	25	10	US-09-821-984-42	Sequence 42, Appl	910	5	1.5	50	9	US-09-895-793-585	Sequence 6, Appl
838	5	1.5	25	10	US-09-815-108-12	Sequence 12, Appl	911	5	1.5	50	9	US-09-895-793-585	Sequence 585, App
839	5	1.5	25	10	US-09-864-761-38662	Sequence 38662, A	912	5	1.5	50	9	US-09-895-814-585	Sequence 585, App
840	5	1.5	25	10	US-09-864-761-45597	Sequence 45597, A	913	5	1.5	50	9	US-10-097-065-376	Sequence 376, App
841	5	1.5	25	10	US-09-938-315-45	Sequence 45, Appl	914	5	1.5	50	10	US-09-759-143-585	Sequence 585, App
842	5	1.5	25	10	US-09-772-719-53	Sequence 53, Appl	915	5	1.5	50	10	US-09-864-761-45994	Sequence 45994, A
843	5	1.5	26	9	US-10-097-065-431	Sequence 431, App	916	5	1.5	50	10	US-09-780-669-585	Sequence 585, App
844	5	1.5	26	10	US-09-870-162A-25	Sequence 25, Appl	917	5	1.5	51	9	US-10-093-200A-5	Sequence 5, Appl
845	5	1.5	26	10	US-09-864-761-37585	Sequence 37585, A	918	5	1.5	52	9	US-09-774-639-258	Sequence 258, App
846	5	1.5	26	10	US-09-864-761-41715	Sequence 41715, A	919	5	1.5	52	9	US-09-969-730-315	Sequence 315, App
847	5	1.5	27	9	US-10-223-047-23	Sequence 23, Appl	920	5	1.5	52	9	US-10-083-357-1158	Sequence 1158, Ap
848	5	1.5	27	9	US-10-097-065-439	Sequence 439, App	921	5	1.5	52	10	US-09-864-761-37509	Sequence 37509, A
849	5	1.5	27	9	US-10-097-065-440	Sequence 440, App	922	5	1.5	53	10	US-09-864-761-33447	Sequence 33447, A
850	5	1.5	28	10	US-09-864-761-34499	Sequence 34499, A	923	5	1.5	53	10	US-09-864-761-46621	Sequence 46621, A
851	5	1.5	28	10	US-09-864-761-46907	Sequence 46907, A	924	5	1.5	53	10	US-09-864-761-48039	Sequence 48039, A
852	5	1.5	29	10	US-09-729-835-95	Sequence 95, Appl	925	5	1.5	53	10	US-09-864-761-48039	Sequence 48039, A
853	5	1.5	29	10	US-09-752-724-8	Sequence 8, Appl	926	5	1.5	53	10	US-09-873-880-12	Sequence 12, Appl
854	5	1.5	30	10	US-09-864-761-34443	Sequence 34443, A	927	5	1.5	54	9	US-09-071-838-178	Sequence 178, App
855	5	1.5	30	10	US-09-864-761-40820	Sequence 40820, A	928	5	1.5	54	10	US-09-756-692-1101	Sequence 1101, Ap
856	5	1.5	30	10	US-09-864-761-45392	Sequence 45392, A	929	5	1.5	54	10	US-09-864-761-43048	Sequence 43048, A
857	5	1.5	32	10	US-09-752-724-6	Sequence 6, Appl	930	5	1.5	54	12	US-10-016-768-3	Sequence 21, Appl
858	5	1.5	32	10	US-09-864-761-35733	Sequence 35733, A	931	5	1.5	55	10	US-09-864-761-35539	Sequence 35539, A
859	5	1.5	32	10	US-09-864-761-46491	Sequence 46491, A	932	5	1.5	55	12	US-10-001-879-172	Sequence 172, App
860	5	1.5	33	10	US-09-737-379-7	Sequence 7, Appl	933	5	1.5	56	9	US-09-902-941-1885	Sequence 1885, Ap
861	5	1.5	33	10	US-09-864-761-46125	Sequence 46125, A	934	5	1.5	56	9	US-09-796-692-2432	Sequence 2432, Ap
862	5	1.5	33	10	US-09-864-761-46457	Sequence 46457, A	935	5	1.5	56	9	US-09-849-826-1885	Sequence 1885, Ap
863	5	1.5	33	10	US-09-864-761-47356	Sequence 47356, A	936	5	1.5	56	9	US-10-017-754-1885	Sequence 1885, Ap
864	5	1.5	34	10	US-09-864-761-36562	Sequence 36562, A	937	5	1.5	56	10	US-09-864-761-44380	Sequence 44380, A
865	5	1.5	34	10	US-09-864-761-45967	Sequence 45967, A	938	5	1.5	56	10	US-09-864-761-48411	Sequence 48411, A
866	5	1.5	35	10	US-09-864-761-38264	Sequence 38264, A	939	5	1.5	57	9	US-09-989-920-227	Sequence 227, App
867	5	1.5	36	9	US-09-869-391-736	Sequence 736, App	940	5	1.5	57	9	US-09-874-056-3	Sequence 3, Appl
868	5	1.5	37	9	US-09-967-237-6	Sequence 6, Appl	941	5	1.5	57	9	US-09-874-056-4	Sequence 4, Appl
869	5	1.5	37	9	US-10-136-703-7	Sequence 7, Appl	942	5	1.5	57	9	US-10-091-504-898	Sequence 898, App
870	5	1.5	37	9	US-10-136-703-34	Sequence 34, Appl	943	5	1.5	57	10	US-09-864-761-37634	Sequence 37634, A
871	5	1.5	37	9	US-10-136-703-35	Sequence 35, Appl	944	5	1.5	57	10	US-09-764-869-898	Sequence 898, App
872	5	1.5	37	9	US-10-136-703-36	Sequence 36, Appl	945	5	1.5	57	10	US-09-764-877-2041	Sequence 2041, Ap
873	5	1.5	37	9	US-10-136-703-37	Sequence 37, Appl	946	5	1.5	58	9	US-09-874-056-5	Sequence 5, Appl
874	5	1.5	37	10	US-09-772-719-6	Sequence 6, Appl	947	5	1.5	58	9	US-09-874-056-7	Sequence 7, Appl
875	5	1.5	38	10	US-09-864-761-36955	Sequence 36955, A	948	5	1.5	58	9	US-10-016-157A-172	Sequence 172, App
876	5	1.5	38	10	US-09-864-761-44495	Sequence 44495, A	949	5	1.5	58	9	US-10-116-235-37	Sequence 37, Appl
877	5	1.5	38	10	US-09-864-761-46302	Sequence 46302, A	950	5	1.5	58	10	US-09-739-254-98	Sequence 98, Appl
878	5	1.5	39	9	US-09-843-676-23	Sequence 23, Appl	951	5	1.5	58	10	US-09-904-615-98	Sequence 98, Appl
879	5	1.5	39	9	US-09-766-253-23	Sequence 23, Appl	952	5	1.5	58	10	US-09-864-761-34517	Sequence 34517, A
880	5	1.5	39	9	US-09-438-486-23	Sequence 23, Appl	953	5	1.5	58	10	US-09-867-852-96	Sequence 96, Appl
881	5	1.5	39	9	US-10-053-758-23	Sequence 23, Appl	954	5	1.5	59	9	US-09-874-056-6	Sequence 6, Appl
882	5	1.5	39	9	US-10-054-295-23	Sequence 23, Appl	955	5	1.5	59	10	US-09-864-761-41455	Sequence 41455, A
883	5	1.5	39	9	US-10-054-611-33	Sequence 23, Appl	956	5	1.5	59	10	US-09-864-761-1381	Sequence 1381, Ap
884	5	1.5	39	10	US-09-864-761-39503	Sequence 39503, A	957	5	1.5	59	10	US-09-895-913A-192	Sequence 192, App
885	5	1.5	40	9	US-10-083-357-1053	Sequence 1053, Ap	958	5	1.5	60	9	US-10-012-896-586	Sequence 586, App
886	5	1.5	41	9	US-09-864-761-36039	Sequence 36039, A	959	5	1.5	60	9	US-10-012-896-886	Sequence 886, App
887	5	1.5	41	9	US-09-922-199A-13	Sequence 13, Appl	960	5	1.5	60	9	US-10-012-896-892	Sequence 892, App
888	5	1.5	41	9	US-09-948-820-47	Sequence 47, Appl	961	5	1.5	60	9	US-09-895-793-586	Sequence 586, App
889	5	1.5	41	10	US-09-864-761-40165	Sequence 40165, A	962	5	1.5	60	9	US-09-895-793-886	Sequence 886, App
890	5	1.5	42	10	US-09-864-761-45355	Sequence 45355, A	963	5	1.5	60	9	US-09-895-793-892	Sequence 892, App
891	5	1.5	42	10	US-09-870-162A-24	Sequence 24, Appl	964	5	1.5	60	9	US-09-895-814-586	Sequence 586, App
892	5	1.5	42	10	US-09-864-761-46961	Sequence 46961, A	965	5	1.5	60	9	US-09-895-814-886	Sequence 886, App
893	5	1.5	42	10	US-09-764-860-492	Sequence 492, App	966	5	1.5	60	9	US-09-895-814-892	Sequence 892, App
894	5	1.5	42	10	US-09-848-664-12	Sequence 12, Appl	967	5	1.5	60	10	US-09-759-143-586	Sequence 586, App
895	5	1.5	42	10	US-09-848-664-13	Sequence 13, Appl	968	5	1.5	60	10	US-09-759-143-886	Sequence 886, App





; SOFTWARE: PatentIn ver. 3.0

; SEQ ID NO 3880

; LENGTH: 191

; TYPE: PRT

; ORGANISM: Corynebacterium glutamicum

US-09-738-626-3880

Query Match

; Sequence 54, Application US/09965703

; Best Local Similarity 100.0%; Pred. No. 6.7;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 APAPAPAP 206

Db 115 APAPAPAP 122

RESULT 7

US-09-965-703-54

; Sequence 54, Application US/09965703

; Patent No. US20020119521A1

; GENERAL INFORMATION:

; APPLICANT: Rohm and Haas Company

; APPLICANT: Palli, Subba Reddy

; APPLICANT: Kapitskaya, Marianna Zinovjevna

; APPLICANT: Cress, Dean Ervin

; TITLE OF INVENTION: No. US20020119521A1el Ecdysone Receptor-Based Inducible Gene Expr

; FILE REFERENCE: A010208

; CURRENT APPLICATION NUMBER: US/09/965,703

; CURRENT FILING DATE: 2001-09-26

; PRIOR APPLICATION NUMBER: 60/191,355

; PRIOR FILING DATE: 2000-03-22

; PRIOR APPLICATION NUMBER: 60/269,799

; PRIOR FILING DATE: 2001-02-20

; PRIOR APPLICATION NUMBER: PCT/US01/09050

; PRIOR FILING DATE: 2001-03-21

; NUMBER OF SEQ ID NOS: 75

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 54

; LENGTH: 269

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-965-703-54

Query Match

; Sequence 50, Application US/10042417

; Best Local Similarity 100.0%; Pred. No. 9.1;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 APAPAPAP 206

Db 108 APAPAPAP 115

RESULT 8

US-10-042-417-50

; Sequence 50, Application US/10042417

; Patent No. US20020123082A1

; GENERAL INFORMATION:

; APPLICANT: pagano, M.

; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF

; TITLE OF INVENTION: PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS

; FILE REFERENCE: 5914-090-999

; CURRENT APPLICATION NUMBER: US/10/042,417

; CURRENT FILING DATE: 2002-01-07

; PRIOR APPLICATION NUMBER: 60/260,179

; PRIOR FILING DATE: 2001-01-5

; NUMBER OF SEQ ID NOS: 89

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 50

; LENGTH: 283

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-042-417-50

Query Match

; Sequence 1040, Application US/09764868

; Best Local Similarity 100.0%; Pred. No. 9.5;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 APAPAPAP 206

Db 3 APAPAPAP 10

RESULT 9

US-09-764-868-1040

; Sequence 1040, Application US/09764868

; Patent No. US20020168711A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PZ32

; CURRENT APPLICATION NUMBER: US/09/764,868

; CURRENT FILING DATE: 2001-01-17

; Prior application data removed - refer to PALM or file wrapper

; NUMBER OF SEQ ID NOS: 1510

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1040

; LENGTH: 332

; TYPE: PRT

; ORGANISM: Homo sapiens

; NAME/KEY: SITE

; LOCATION: (72)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (81)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (89)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (91)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (106)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (270)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (275)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (280)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (283)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (307)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (313)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (321)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (329)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (329)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (329)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (329)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (329)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (329)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (329)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

RESULT 12  
US-09-771-161A-273  
; Sequence 273, Application US/09771161A  
; Patent No. US2002011081A1  
; GENERAL INFORMATION:



US-09-298-523B-62

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Best Local Similarity 100.0%; Pred. No. 22;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 200 PAPAPAPE 207  
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Db 646 PAPAPAPE 653

RESULT 15

US-09-298-523B-2  
; Sequence 2, Application US/09298523B  
; Publication No. US20030059438A1  
; GENERAL INFORMATION:  
; APPLICANT: BRILES et al.  
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPITOPIC REGIONS  
; FILE REFERENCE: 454312-3140  
; CURRENT APPLICATION NUMBER: US/09/298,523B  
; CURRENT FILING DATE: 1999-04-23  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 707  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-09-298-523B-2

Query Match 2.3%; Score 8; DB 9; Length 707;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 200 PAPAPAPE 207  
|||||||  
Db 647 PAPAPAPE 654

Search completed: April 15, 2003, 09:03:33  
Job time : 38 secs

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: April 15, 2003, 08:53:24 ; Search time 18 Seconds  
(without alignments):  
1837.236 Million cell updates/sec

Title: US-09-831-061-2

Perfect score: 344

Sequence: 1 MKAIFVLNAAPKDNWTYAGG.....DRRVEIEVKGKVVTPAG 344

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Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

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1: PIR1:\*

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3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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1	335	97.4	356	2	JC6558
2	53	15.4	238	2	outer membrane pro
3	53	15.4	350	2	outer membrane pro
4	43	12.5	238	2	outer membrane pro
5	33	9.6	346	1	MNECA
6	33	9.6	346	2	outer membrane pro
7	33	9.6	346	2	outer membrane pro
8	29	8.4	243	2	outer membrane pro
9	29	8.4	243	2	outer membrane pro
10	29	8.4	244	2	outer membrane pro
11	27	7.8	243	2	outer membrane pro
12	27	7.8	243	2	outer membrane pro
13	24	7.0	351	1	MNEBAC
14	22	6.4	350	1	MNEBAC
15	22	6.4	350	2	outer membrane pro
16	22	6.4	353	2	outer membrane pro
17	20	5.8	240	2	outer membrane pro
18	20	5.8	241	2	outer membrane pro
19	20	5.8	241	2	outer membrane pro
20	19	5.5	359	2	outer membrane pro
21	12	3.5	349	2	outer membrane pro
22	9	2.6	187	2	outer membrane pro
23	9	2.6	193	1	MORT4E
24	9	2.6	197	1	MOHU4E
25	9	2.6	215	2	S55925
26	9	2.6	383	2	A43470
27	9	2.6	458	2	H82051
28	9	2.6	581	2	T22341
29	9	2.6	1061	1	S27311

30	1061	2	F90811	RNase E [imported]
31	1061	2	B85671	RNase E [similarit
32	1785	2	A45546	major merizote su
33	1895	2	T15881	hypothetical prote
34	3869	2	A48205	All-i protein +GPE
35	28	2	A60752	outer membrane pro
36	51	2	B27191	nonhistone chromos
37	84	2	T23177	hypothetical prote
38	94	2	C90744	hypothetical prote
39	94	2	G85594	hypothetical prote
40	129	2	D49094	YbjH protein, precu
41	134	2	T44984	methymalonyl-CoA
42	145	2	T33037	hypothetical prote
43	163	2	D87519	glcG protein, prob
44	165	2	S35195	hypothetical prote
45	182	2	C87097	conserved hypotet
46	188	2	A32553	myosin Al catalyti
47	189	2	I57590	myosin light chain
48	190	1	MORT41	myosin alkali ligh
49	190	2	T25482	hypothetical prote
50	192	1	MORBLA	myosin alkali ligh
51	192	1	MOHUA1	myosin alkali ligh
52	194	1	MOHUA1	hypothetical prote
53	208	2	A87269	beta-crystallin B1
54	208	2	D87312	hypothetical prote
55	216	2	G70555	conserved hypotet
56	227	2	G70555	hypothetical prote
57	240	2	S75318	hypothetical prote
58	241	2	T51206	ferripyochelin-bin
59	253	2	S07264	hypothetical prote
60	254	2	D84461	hypothetical prote
61	261	2	JN0747	outer membrane pro
62	313	1	RBSMHP	histone H1-I - vol
63	316	2	G02424	mammosyl-glycoprot
64	331	2	B40951	cyclin-dependent k
65	344	2	S46745	TiF1 protein - mou
66	346	2	T46916	hypothetical prote
67	353	2	C64187	outer membrane pro
68	361	2	T30402	hypothetical prote
69	379	2	T14337	RAD23 protein, iso
70	399	2	E91220	uroporphyrinogen I
71	399	2	G86066	uroporphyrinogen I
72	416	1	SKLALG	dermal gland prote
73	424	2	T29158	hypothetical prote
74	437	2	I51238	translation elonga
75	438	2	G87675	arylesterase-relat
76	500	2	C75341	tetradicopeptide
77	537	2	I53719	NF-kappa-B transcr
78	550	2	A42017	transcription fact
79	551	2	A40851	transforming prote
80	552	2	T08148	proline-rich myros
81	553	2	B55514	dihydrolipoamide S
82	582	2	A87316	hypothetical prote
83	584	2	H87304	hypothetical prote
84	590	1	T35297	probable dihydrol
85	596	2	A28088	oxaloacetate decar
86	596	2	F75302	ATP-dependent DNA
87	600	2	C82221	transport protein
88	642	2	A96560	hypothetical prote
89	676	1	EDBE22	immediate-early pr
90	676	1	EDBE23	immediate-early pr
91	676	2	T34609	probable tpr prote
92	693	2	G71302	hypothetical prote
93	698	2	T51915	hypothetical prote
94	747	2	T23607	hypothetical prote
95	963	2	T40290	hypothetical prote
96	1023	2	B59430	KiRA0189 protein [
97	1051	2	S55259	TiF1 protein - mou
98	1097	2	T31504	hypothetical prote
99	1151	2	T18535	high molecular mas
100	1174	2	T49868	related to suppres
101	1385	2	T14158	neurexin IV - mous
102	1513	2	T23681	hypothetical prote

103	8	2.3	1584	2	T22674	hypothetical prote	176	7	2.0	428	2	A95018	DNA-binding respon
104	8	2.3	1585	2	T31611	hypothetical prote	177	7	2.0	428	2	B97891	response regulator
105	8	2.3	2197	2	B71600	variant-specific s	178	7	2.0	430	2	AG2256	dihydrolipamide s
106	8	2.3	2774	2	A43359	microtubule-associ	179	7	2.0	435	2	T05452	hypothetical prote
107	7	2.0	14	1	LFECW	trp operon leader	180	7	2.0	449	2	J01438	polyprotein - culi
108	7	2.0	14	2	E90858	trp operon leader	181	7	2.0	453	2	S39866	outer membrane pro
109	7	2.0	14	2	A58503	kidney and bladder	182	7	2.0	455	2	A87913	protein B0205.10 [
110	7	2.0	14	2	B85761	trp operon leader	183	7	2.0	457	2	C65203	argininosuccinate
111	7	2.0	66	2	D31844	hypothetical 7.7K	184	7	2.0	457	2	A98240	argininosuccinate
112	7	2.0	66	2	H71635	metallothionein ol	185	7	2.0	457	2	F86087	argininosuccinate
113	7	2.0	105	2	H71635	hypothetical prote	186	7	2.0	457	2	A10477	probable argininos
114	7	2.0	108	2	C72451	hypothetical prote	187	7	2.0	457	2	A51194	cell division prot
115	7	2.0	120	2	AF1646	hypothetical prote	188	7	2.0	457	2	F98060	cell division prot
116	7	2.0	125	2	S34435	protein-tyrosine k	189	7	2.0	457	2	JQ2184	hypothetical 50.4K
117	7	2.0	123	2	S65803	transcription acti	190	7	2.0	458	2	AH0935	argininosuccinate
118	7	2.0	132	2	S07779	copper chaperone h	191	7	2.0	474	2	T38485	centromere/microtu
119	7	2.0	138	2	S52933	major allergen Par	192	7	2.0	478	2	JC4940	synapsin IIB - hum
120	7	2.0	155	2	E64105	acetyl-CoA carboxy	193	7	2.0	486	2	T35445	probable integral
121	7	2.0	171	2	B96548	probable proline-r	194	7	2.0	493	2	B48362	transcription init
122	7	2.0	200	1	A71127	hypothetical prote	195	7	2.0	507	2	S05542	hypothetical prote
123	7	2.0	207	2	C84631	nodulin-like prote	196	7	2.0	515	2	S39731	pyroline-5 carbox
124	7	2.0	208	2	A43696	Spec3 protein - se	197	7	2.0	524	2	A75588	probable protein k
125	7	2.0	210	2	AG0534	hypothetical prote	198	7	2.0	527	1	S25481	heat shock transcr
126	7	2.0	212	2	H75317	translation initia	199	7	2.0	528	2	D46449	hypothetical prote
127	7	2.0	212	2	T47918	probable DNA-bindi	200	7	2.0	551	2	F83015	hypothetical prote
128	7	2.0	213	2	T03931	DNA binding protei	201	7	2.0	556	2	D70940	probable PPE prote
129	7	2.0	222	2	H96711	hypothetical prote	202	7	2.0	568	2	E75502	threonine ammonia-
130	7	2.0	223	2	F71439	probable serine pr	203	7	2.0	574	2	F75356	serine/threonine p
131	7	2.0	228	2	S46965	microfilament shea	204	7	2.0	574	2	T43556	Wiskott-Aldrich sy
132	7	2.0	236	2	AH1630	B. subtilis late c	205	7	2.0	574	2	T38819	Wiskott-Aldrich sy
133	7	2.0	238	2	S66358	DNA-binding protei	206	7	2.0	586	2	S65802	transcription acti
134	7	2.0	246	2	T48338	arabinogalactan pr	207	7	2.0	587	2	B83015	arganyl-tRNA synth
135	7	2.0	252	2	T04739	hypothetical prote	208	7	2.0	587	2	E87420	poly-beta-hydroxyb
136	7	2.0	256	2	T10376	hypothetical prote	209	7	2.0	587	2	E85429	hypothetical prote
137	7	2.0	261	2	B81823	Deda-family integr	210	7	2.0	594	1	D55514	dihydrolipamide d
138	7	2.0	262	2	B75365	hypothetical prote	211	7	2.0	595	2	T49384	related to NR01 pr
139	7	2.0	265	2	AG2084	ABC transporter, A	212	7	2.0	606	2	T51880	hypothetical prote
140	7	2.0	265	2	D97632	hypothetical prote	213	7	2.0	632	2	S42629	keratin K3 - rabbi
141	7	2.0	265	2	AG2855	conserved hypotet	214	7	2.0	639	2	C98264	S'-nucleotidase pr
142	7	2.0	279	2	C96721	hypothetical prote	215	7	2.0	636	2	AF3020	S'-nucleotidase [1
143	7	2.0	289	2	S56287	hypothetical prote	216	7	2.0	640	2	G70573	probable transmemb
144	7	2.0	289	2	T03395	probable lipase -	217	7	2.0	643	2	T23453	hypothetical prote
145	7	2.0	296	2	T46619	hypothetical prote	218	7	2.0	648	2	C69423	DNA helicase homol
146	7	2.0	297	2	S23737	proline-rich prote	219	7	2.0	691	2	T15983	hypothetical prote
147	7	2.0	307	2	D97605	proteinase chain h	220	7	2.0	700	2	B82788	hypothetical prote
148	7	2.0	307	2	AF2827	HFCL protein limpo	221	7	2.0	703	2	D81365	metalloproteinase x
149	7	2.0	311	2	H70511	hypothetical prote	222	7	2.0	729	2	E70803	hypothetical prote
150	7	2.0	321	2	F82104	outer membrane pro	223	7	2.0	757	2	A99561	conserved hypotet
151	7	2.0	325	2	D70666	probable modb prot	224	7	2.0	766	1	S61694	flocculation suppr
152	7	2.0	328	2	T37734	SUR4 family protei	225	7	2.0	790	1	FOVWH2	gag-kit polyprotei
153	7	2.0	329	2	A37864	SQL protein homolo	226	7	2.0	799	2	T48889	serine/threonine p
154	7	2.0	331	2	A36358	T-cell acute lymph	227	7	2.0	801	2	T29018	hypothetical prote
155	7	2.0	337	2	S55932	NCA3 protein precu	228	7	2.0	809	2	A57283	integrin beta chal
156	7	2.0	345	2	S12788	transcription fact	229	7	2.0	811	2	T36581	probable transmemb
157	7	2.0	347	2	H75253	hypothetical prote	230	7	2.0	815	2	B56708	extracellular sign
158	7	2.0	348	2	D75357	hypothetical prote	231	7	2.0	833	2	AF2089	hypothetical prote
159	7	2.0	351	1	VCNVP1	major capsid prote	232	7	2.0	852	2	S28415	guanine nucleotide
160	7	2.0	351	2	T10359	p39 capsid protei	233	7	2.0	873	2	A47283	calpottin - fruit
161	7	2.0	354	2	AB0842	glycine betaine/L-	234	7	2.0	892	2	H71558	probable translati
162	7	2.0	356	2	A13648	flagellar biosynth	235	7	2.0	907	2	AB1885	hypothetical prote
163	7	2.0	362	2	JU0353	hypothetical 39.7K	236	7	2.0	913	2	B97369	translation initia
164	7	2.0	362	2	T45072	erythroid Kruppel-	237	7	2.0	913	2	AB2587	translation initia
165	7	2.0	365	2	B75398	hypothetical prote	238	7	2.0	932	2	T25941	hypothetical prote
166	7	2.0	366	2	B84712	probable protean k	239	7	2.0	950	2	B44766	defective chorion-
167	7	2.0	375	2	F75467	probable lipoprote	240	7	2.0	954	2	I51703	c-kit-related kina
168	7	2.0	379	2	T40384	probable methionin	241	7	2.0	960	1	JN0677	protein-tyrosine k
169	7	2.0	388	2	T35170	hypothetical prote	242	7	2.0	972	1	TVHUMD	macrophage colony-
170	7	2.0	407	2	A85191	probable serine pr	243	7	2.0	975	1	TVMSKT	protein-tyrosine k
171	7	2.0	407	2	B83143	probable hydrolase	244	7	2.0	975	2	T30816	macrophage colony-
172	7	2.0	413	2	JC2135	chitinase (EC 3.2.	245	7	2.0	976	1	TVMSMD	macrophage colony-
173	7	2.0	425	2	D84298	histidinol dehydro	246	7	2.0	976	1	TVHUKT	protein-tyrosine k
174	7	2.0	426	2	E97445	nitrate transport	247	7	2.0	977	2	I45877	protein-tyrosine k
175	7	2.0	426	2	AF2663	hypothetical prote	248	7	2.0	978	1	A49814	protein-tyrosine k

249	7	2.0	978	2	S16385	macrophage colony-	322	1.7	122	2	I38081	gene p27 protein -
250	7	2.0	980	1	TUCTMD	macrophage colony-	323	1.7	123	2	AD0039	diacylglycerol kin
251	7	2.0	995	2	T32466	hypothetical prote	324	1.7	123	2	B69351	hypothetical prote
252	7	2.0	1016	2	H71460	probable outer mem	325	1.7	124	2	C82805	DNA-binding protei
253	7	2.0	1087	2	T30844	serine-repeat anti	326	1.7	125	2	G75265	probable protein t
254	7	2.0	1095	1	A31225	phospholipase C (E	327	1.7	128	2	A29349	hypothetical prote
255	7	2.0	1111	2	T29070	hypothetical prote	328	1.7	129	2	AG2003	hypothetical prote
256	7	2.0	1123	2	A44766	defective chorion-	329	1.7	130	2	A71530	ribosomal protein
257	7	2.0	1125	1	F70177	transcription-repa	330	1.7	130	2	H81584	ribosomal protein
258	7	2.0	1131	2	S22266	FUN30 protein - ye	331	1.7	130	2	E70585	probable furB prot
259	7	2.0	1132	2	C75259	probable iron-sulf	332	1.7	130	2	S65804	transcription acti
260	7	2.0	1147	1	MXAXIB	myosin heavy chain	333	1.7	131	2	A84613	hypothetical prote
261	7	2.0	1149	2	T27567	hypothetical prote	334	1.7	132	2	T11239	hypothetical prote
262	7	2.0	1239	1	Q0BE10	BOLFI protein - hu	335	1.7	133	2	T42978	hypothetical prote
263	7	2.0	1274	2	S55050	cardiac myosin-bin	336	1.7	136	2	S74785	hypothetical prote
264	7	2.0	1298	2	A48929	protein-tyrosine k	337	1.7	137	2	T03491	conserved hypochet
265	7	2.0	1323	2	E86257	protein let-23 (im	338	1.7	138	2	AE1324	PTB mannose-specif
266	7	2.0	1374	2	S70712	protein-tyrosine k	339	1.7	139	2	H70784	PTB mannose-specif
267	7	2.0	1464	2	S58984	development protei	340	1.7	140	2	S74072	hypothetical prote
268	7	2.0	1487	1	EDBE81	immediate-early pr	341	1.7	141	2	D82745	hypothetical prote
269	7	2.0	1589	2	C44766	155K transcription	342	1.7	142	2	B69515	hypothetical prote
270	7	2.0	1618	2	S21434	defective chorion-	343	1.7	142	2	B69515	hypothetical prote
271	7	2.0	2156	1	RRVUNE	nestin - human	344	1.7	147	2	T31442	probable cytochrom
272	7	2.0	2408	2	T24483	genome polyprotein	345	1.7	149	2	E83633	hypothetical prote
273	7	2.0	2649	2	T51023	hypothetical prote	346	1.7	151	2	AE3643	adhesin a1a-I (im
274	6	1.7	35	2	H81948	hypothetical prote	347	1.7	153	2	AE7400	conserved hypotet
275	6	1.7	38	1	HSPV5	histone H5 - pigeo	348	1.7	154	2	S64076	probable membrane
276	6	1.7	40	2	S77777	hypothetical prote	349	1.7	155	2	B82783	hypothetical prote
277	6	1.7	46	2	S07073	hypothetical prote	350	1.7	156	2	B87509	hypothetical prote
278	6	1.7	48	2	AD2809	arabinogalactan pr	351	1.7	158	2	AI2377	conserved hypotet
279	6	1.7	67	2	B83792	hypothetical prote	352	1.7	158	2	T02973	lipoprotein signal
280	6	1.7	68	2	B84050	small acid-soluble	353	1.7	158	2	B71096	probenazole-induce
281	6	1.7	70	2	T31845	hypothetical prote	354	1.7	158	2	D75069	hypothetical prote
282	6	1.7	72	1	C48380	small acid-soluble	355	1.7	159	2	F72754	hypothetical prote
283	6	1.7	73	2	E84901	hypothetical prote	356	1.7	161	2	S78002	hypothetical prote
284	6	1.7	73	2	B82540	hypothetical prote	357	1.7	162	2	C81808	cuticle structural
285	6	1.7	74	2	G82810	hypothetical prote	358	1.7	163	2	C91092	hypothetical prote
286	6	1.7	74	2	G81370	hypothetical prote	359	1.7	163	2	B85937	hypothetical prote
287	6	1.7	75	2	T26916	probable periplasm	360	1.7	164	2	B82800	hypothetical prote
288	6	1.7	79	2	AG3427	hypothetical prote	361	1.7	165	2	A90169	hypothetical prote
289	6	1.7	82	2	F81521	transposase BME14	362	1.7	166	2	G85057	hypothetical prote
290	6	1.7	82	2	F75326	conserved hypotet	363	1.7	167	2	B43871	probable transposa
291	6	1.7	86	2	F97124	phosphocarrier Pro	364	1.7	168	2	JC5192	hypothetical prote
292	6	1.7	88	2	S38267	cuticle protein Lm	365	1.7	168	2	T34804	hypothetical prote
293	6	1.7	89	2	A84450	hypothetical prote	366	1.7	168	2	AE0055	hypothetical prote
294	6	1.7	90	2	A96505	probable glycine-r	367	1.7	169	2	T04162	hypothetical prote
295	6	1.7	90	2	G82452	conserved hypotet	368	1.7	169	2	E95005	probable lipoprote
296	6	1.7	92	1	WMNVPM	protein p10 - Orgy	369	1.7	169	2	B97878	hemoglobin 2 - ric
297	6	1.7	92	1	T10402	hypothetical prote	370	1.7	170	2	G70638	telocoplanin resist
298	6	1.7	94	2	AG0556	phosphoenolpyruvat	371	1.7	172	2	S62167	hypothetical prote
299	6	1.7	95	2	T34569	hypothetical prote	372	1.7	173	2	S44407	NADH2 dehydrogenas
300	6	1.7	100	2	T17126	hypothetical prote	373	1.7	173	2	S44405	NADH2 dehydrogenas
301	6	1.7	104	2	AI2257	hypothetical prote	374	1.7	173	2	S44398	NADH2 dehydrogenas
302	6	1.7	104	2	E86263	hypothetical prote	375	1.7	173	2	S44413	NADH2 dehydrogenas
303	6	1.7	108	2	D86877	hypothetical prote	376	1.7	173	2	S44414	NADH2 dehydrogenas
304	6	1.7	108	2	B99918	hypothetical prote	377	1.7	173	2	S44399	NADH2 dehydrogenas
305	6	1.7	109	2	G69276	conserved hypotet	378	1.7	173	2	S44396	NADH2 dehydrogenas
306	6	1.7	113	2	S77123	ribosomal protein	379	1.7	173	2	S44412	NADH2 dehydrogenas
307	6	1.7	115	2	JQ1885	V2 protein - tomat	380	1.7	173	2	S44410	NADH2 dehydrogenas
308	6	1.7	115	2	AF1044	periplasmic divale	381	1.7	173	2	S44409	NADH2 dehydrogenas
309	6	1.7	118	1	R7MCML	ribosomal protein	382	1.7	173	2	S44400	NADH2 dehydrogenas
310	6	1.7	118	2	B90259	hypothetical prote	383	1.7	173	2	S44402	NADH2 dehydrogenas
311	6	1.7	118	2	AB0282	hypothetical prote	384	1.7	173	2	S44406	NADH2 dehydrogenas
312	6	1.7	119	2	A85654	probable diacygly	385	1.7	173	2	S44411	NADH2 dehydrogenas
313	6	1.7	119	2	D90793	probable diacygly	386	1.7	173	2	S34633	NADH2 dehydrogenas
314	6	1.7	120	2	C75563	hypothetical prote	387	1.7	173	2	E90613	NADH2 dehydrogenas
315	6	1.7	121	2	S65793	catalase (EC 1.11.	388	1.7	173	2	E90615	NADH dehydrogenase
316	6	1.7	121	2	D86468	hypothetical prote	389	1.7	173	2	E90621	NADH dehydrogenase
317	6	1.7	122	1	KIECDG	probable diacygly	390	1.7	173	2	E90625	NADH dehydrogenase
318	6	1.7	122	2	AG1257	diacylglycerol kin	391	1.7	173	2	T11531	NADH2 dehydrogenas
319	6	1.7	122	2	AC1015	diacylglycerol kin	392	1.7	173	2	T11034	NADH2 dehydrogenas
320	6	1.7	122	2	E86097	diacylglycerol kin	393	1.7	173	2	H90003	ATP synthase B cha
321	6	1.7	122	2	E86097	diacylglycerol kin	394	1.7	174	2	E90617	NADH dehydrogenase

395	6	1.7	174	2	F97240	peptidyl-prolyl ci	468	1.7	222	2	A75406	hydrolase - Deinoc
396	6	1.7	174	2	B65046	hypothetical prote	469	1.7	222	2	A99884	phage shock protei
397	6	1.7	175	2	T11179	NADH2 dehydrogenas	470	1.7	222	2	H82169	phage shock protei
398	6	1.7	175	2	A37786	pituitary adenylat	471	1.7	222	2	AF0658	phage shock protei
399	6	1.7	175	2	B72496	hypothetical prote	472	1.7	222	2	H85754	phage shock protei
400	6	1.7	178	2	G95090	conserved hypotet	473	1.7	222	2	C64879	phage shock protei
401	6	1.7	178	2	C97958	biotin synthase (E	474	1.7	223	2	H87335	conserved hypotet
402	6	1.7	179	2	S30994	gene 49 protein -	475	1.7	223	2	C82230	probable lipoprote
403	6	1.7	183	2	T51910	hypothetical prote	476	1.7	223	2	E89567	protein T08A9.9 [I
404	6	1.7	183	2	C90212	conserved hypotet	477	1.7	224	2	B72040	coenzyme pqq synth
405	6	1.7	186	2	C41132	collagen-related p	478	1.7	224	2	G86585	crf610 hypotetical
406	6	1.7	187	2	S24992	photosystem II pro	479	1.7	226	2	T19891	2-haloacid dehalog
407	6	1.7	188	2	T31526	hypothetical prote	480	1.7	227	2	A38452	extensin-like prot
408	6	1.7	189	2	T36207	probable alanine-r	481	1.7	227	2	S53504	hypothetical prote
409	6	1.7	191	2	JQ1919	hypothetical prote	482	1.7	228	2	T20777	probable ABC trans
410	6	1.7	192	2	A56141	hypothetical 21.3K	483	1.7	230	2	D75518	probable ABC trans
411	6	1.7	192	2	A12271	ribonuclease H (EC	484	1.7	230	2	E72470	oxidase [Imported]
412	6	1.7	193	1	HS655	histone H5 - goose	485	1.7	230	2	AB2068	hypothetical prote
413	6	1.7	193	1	HS722	transcription regu	486	1.7	230	2	B83060	cuticular protein
414	6	1.7	194	1	HSTR1	transcription regu	487	1.7	231	2	T12012	transforming prote
415	6	1.7	194	2	S07260	histone H1 - trout	488	1.7	231	2	S24390	plasma membrane pr
416	6	1.7	194	2	A45275	histone H5 - musco	489	1.7	232	2	T03678	conserved hypotet
417	6	1.7	195	1	MOHU3V	21K outer membrane	490	1.7	232	2	D87623	exotoxin 12 [impor
418	6	1.7	196	1	A42377	myosin alkali ligh	491	1.7	232	2	E89807	hypothetical prote
419	6	1.7	197	2	F75468	hypothetical prote	492	1.7	232	2	B90210	transforming prote
420	6	1.7	197	2	D70017	probable DNA polym	493	1.7	233	2	A37332	hypothetical prote
421	6	1.7	197	2	C82601	hypothetical prote	494	1.7	233	2	S05032	hypothetical prote
422	6	1.7	197	2	H86979	hypothetical prote	495	1.7	233	2	F70606	probable pkmw prot
423	6	1.7	199	2	JU0052	hypothetical prote	496	1.7	237	2	A42013	alpha-1-B-glycopro
424	6	1.7	199	2	C69659	puromycin N-acetyl	497	1.7	237	2	CYCHB1	beta-crystallin B1
425	6	1.7	199	2	T14468	molybdopterin-guan	498	1.7	238	1	AC2013	hypothetical prote
426	6	1.7	201	2	A0283	pollen coat protei	499	1.7	238	2	T28419	thiamin-phosphate
427	6	1.7	201	2	H70635	lacyl-carrier-prot	500	1.7	238	2	F98066	hypothetical prote
428	6	1.7	201	2	E95072	nitroreductase fam	501	1.7	240	2	H64373	hypothetical prote
429	6	1.7	201	2	B97940	nitroreductase (EC	502	1.7	240	2	SL9999	hypothetical prote
430	6	1.7	201	2	S54475	hypothetical prote	503	1.7	241	2	D87494	conserved hypotet
431	6	1.7	201	2	B81421	hypothetical prote	504	1.7	241	2	S53522	crystallin beta B1
432	6	1.7	202	2	S76439	endopeptidase Clp	505	1.7	241	2	G98156	hypothetical prote
433	6	1.7	202	2	F84382	hypothetical prote	506	1.7	243	2	B95885	hypothetical prote
434	6	1.7	203	2	S00747	hypothetical prote	507	1.7	243	2	T20810	hypothetical prote
435	6	1.7	203	2	A72705	somatotropin precu	508	1.7	244	2	A87505	hypothetical prote
436	6	1.7	204	1	STFI	hypothetical prote	509	1.7	244	2	T16942	flagellar L-ring p
437	6	1.7	204	1	IS1289	somatotropin - Mor	510	1.7	245	1	G64834	hypothetical prote
438	6	1.7	204	2	S01746	somatotropin - Aca	511	1.7	245	1	AB2195	probable fibrinoly
439	6	1.7	204	2	S30491	somatotropin precu	512	1.7	245	1	A84289	hypothetical prote
440	6	1.7	204	2	A56904	somatotropin precu	513	1.7	246	1	C72109	hypothetical prote
441	6	1.7	204	2	JC4261	somatotropin precu	514	1.7	246	2	D86512	IMP dehydrogenase
442	6	1.7	204	2	T15274	hypothetical prote	515	1.7	247	2	AB2465	hypothetical prote
443	6	1.7	205	2	B87296	hypothetical prote	516	1.7	249	2	S76547	hypothetical prote
444	6	1.7	205	2	I40812	ribonuclease HII	517	1.7	250	2	T35839	probable dihydrodi
445	6	1.7	206	1	HSTR1R	porphobilinogen sy	518	1.7	250	2	C87489	biotin protein lig
446	6	1.7	208	2	C24723	histone H1 - rainb	519	1.7	250	2	D75364	hypothetical prote
447	6	1.7	208	2	S15091	trpG protein - Cor	520	1.7	250	2	G85015	hypothetical prote
448	6	1.7	208	2	H70965	homeotic protein p	521	1.7	251	2	F83604	hypothetical prote
449	6	1.7	208	2	T36390	probable phage pro	522	1.7	251	2	G97462	hypothetical prote
450	6	1.7	211	2	F71111	hypothetical prote	523	1.7	253	2	B47019	hypothetical prote
451	6	1.7	211	2	T08112	pectinesterase hom	524	1.7	254	2	T36161	Cfxy protein - Alc
452	6	1.7	215	2	AB2253	hypothetical prote	525	1.7	254	2	T25073	hypothetical prote
453	6	1.7	215	2	F82211	probable glutathio	526	1.7	254	2	AB2681	transcription regu
454	6	1.7	215	2	T03680	probable methyltra	527	1.7	255	2	AB2109	phosphatidyltransf
455	6	1.7	215	2	T36448	transforming prote	528	1.7	256	2	G82804	conserved hypotet
456	6	1.7	216	2	B37332	hypothetical prote	529	1.7	256	2	T21238	hypothetical prote
457	6	1.7	216	2	H69797	probable transcrip	530	1.7	256	2	G97031	TPR-repeat contain
458	6	1.7	217	1	G91010	hypothetical prote	531	1.7	257	2	B41843	hypothetical prote
459	6	1.7	219	2	T19897	probable transcrip	532	1.7	258	2	T24035	hypothetical prote
460	6	1.7	219	2	A85855	hypothetical prote	533	1.7	258	2	G96023	probable phosphona
461	6	1.7	219	2	B64985	hypothetical 25.3	534	1.7	259	2	A29831	acid phosphatase I
462	6	1.7	220	2	A46597	acidic calmodulin-	535	1.7	259	2	A13116	heat-labile entero
463	6	1.7	220	2	H90173	3-dehydroquinatate d	536	1.7	259	2	T09415	hypothetical prote
464	6	1.7	221	2	B72318	hypothetical prote	537	1.7	259	2	AC0332	probable surface p
465	6	1.7	221	2	AH0286	phage shock protei	538	1.7	261	2	AF2698	probable OmpA fam1
466	6	1.7	221	2	AB3018	thiamin-phosphate	539	1.7	262	2	AF2698	NAD/NADP dependent
467	6	1.7	221	2	AB3018	thiamin-phosphate	540	1.7	262	2	AF2698	NAD/NADP dependent

541	6	1.7	263	2	T09841	hypothetical prote	614	1.7	298	2	JC7568	kidney inhibitor o
542	6	1.7	264	2	E75161	shikimate 5-dehydr	615	1.7	299	2	A99422	hypothetical prote
543	6	1.7	265	2	AH0759	propanediol diffus	616	1.7	300	2	F97277	probable glycosyl
544	6	1.7	266	2	F97086	anaerobic sulfite	617	1.7	301	2	A75599	ribokinase - Deino
545	6	1.7	267	2	T36461	hypothetical prote	618	1.7	302	2	E97380	phn7 protein [impo
546	6	1.7	268	2	B95988	hypothetical prote	619	1.7	303	2	AD2598	conserved hypothet
547	6	1.7	269	2	D98241	hypothetical prote	620	1.7	304	2	T47557	hypothetical prote
548	6	1.7	270	2	AH3044	conserved hypothet	621	1.7	305	2	H82569	proliporotein dia
549	6	1.7	271	2	R5H07A	ribosomal protein	622	1.7	306	2	B75509	conserved hypothet
550	6	1.7	272	2	S18159	ribosomal protein	623	1.7	307	2	A75509	similar to ABC tra
551	6	1.7	273	2	A30241	ribosomal protein	624	1.7	308	2	B95007	PTS system, IIC co
552	6	1.7	274	2	C90411	ketopantoate hydro	625	1.7	309	2	E97879	hypothetical prote
553	6	1.7	275	2	A87404	ribosomal protein	626	1.7	310	2	D83479	probable transcript
554	6	1.7	276	2	G84319	ribosomal protein	627	1.7	311	2	E97879	transforming prote
555	6	1.7	277	2	F64024	crotonine-5'-monop	628	1.7	312	2	D83479	hypothetical prote
556	6	1.7	278	2	T19829	hypothetical prote	629	1.7	313	2	TVH0UD	probable transcript
557	6	1.7	279	2	H75576	hypothetical prote	630	1.7	314	2	BVECM	transforming prote
558	6	1.7	280	2	T26957	hypothetical prote	631	1.7	315	2	E95855	hypothetical prote
559	6	1.7	281	2	T35961	hypothetical prote	632	1.7	316	2	E95855	conserved hypothet
560	6	1.7	282	2	T30959	phosphoribosylform	633	1.7	317	2	E81288	probable oligopept
561	6	1.7	283	2	A70853	probable transcript	634	1.7	318	2	AD3154	hypothetical prote
562	6	1.7	284	2	H82488	hypothetical prote	635	1.7	319	2	E65112	nucleotidyltransfe
563	6	1.7	285	2	B45247	hypothetical prote	636	1.7	320	2	S25511	hypothetical 34.6
564	6	1.7	286	2	T47937	hypothetical prote	637	1.7	321	2	E91140	outer membrane pro
565	6	1.7	287	2	G75606	probable glycohydr	638	1.7	322	2	E85985	hypothetical prote
566	6	1.7	288	2	A69077	conserved hypothet	639	1.7	323	2	AH0906	hypothetical prote
567	6	1.7	289	2	A70853	hypothetical prote	640	1.7	324	2	B83294	probable ATP-bindi
568	6	1.7	290	2	H82488	hypothetical prote	641	1.7	325	2	E90277	hypothetical prote
569	6	1.7	291	2	B45247	NH(3)-dependent NA	642	1.7	326	2	B87433	probable ATP-bindi
570	6	1.7	292	2	C82273	Arac homolog ToxT	643	1.7	327	2	D69881	hypothetical prote
571	6	1.7	293	2	S32274	tepn protein - Vib	644	1.7	328	2	A61183	sulfate adenylate
572	6	1.7	294	2	A22295	thiosulfate sulfur	645	1.7	329	2	I40491	yabc protein homol
573	6	1.7	295	2	G71849	amino acid ABC tra	646	1.7	330	2	C98193	hypothetical prote
574	6	1.7	296	2	S71222	xyloglucan endo-1,	647	1.7	331	2	AG3093	conserved hypothet
575	6	1.7	297	2	T06613	probable sugar nuc	648	1.7	332	2	B81168	sugar transport sy
576	6	1.7	298	2	A69112	quinolinate phosph	649	1.7	333	2	T06053	hypothetical prote
577	6	1.7	299	2	E89226	hypothetical prote	650	1.7	334	2	C70798	transporter NMB070
578	6	1.7	300	2	F97034	hypothetical prote	651	1.7	335	2	B99607	probable ubiqutin
579	6	1.7	301	2	G84636	hypothetical prote	652	1.7	336	2	C82085	probable PPE prote
580	6	1.7	302	2	D84968	hypothetical prote	653	1.7	337	2	T31880	hypothetical prote
581	6	1.7	303	2	H70942	hypothetical prote	654	1.7	338	2	AG0121	conserved hypothet
582	6	1.7	304	2	S78161	H+-transporting tw	655	1.7	339	2	C70356	hypothetical prote
583	6	1.7	305	2	TU0115	genome polyprotein	656	1.7	340	2	T45591	probable sideropho
584	6	1.7	306	2	A92055	hypothetical prote	657	1.7	341	2	AE1932	conserved hypothet
585	6	1.7	307	2	G88349	sulfate ABC transp	658	1.7	342	2	A93510	probable 35 kDa r1
586	6	1.7	308	2	E88597	protein Y48E1C.1	659	1.7	343	2	A69992	hypothetical prote
587	6	1.7	309	2	T27027	protein Y47D3B.6	660	1.7	344	2	S62810	hypothetical prote
588	6	1.7	310	2	AC2551	hypothetical prote	661	1.7	345	2	A41773	conserved hypothet
589	6	1.7	311	2	D32354	hypothetical prote	662	1.7	346	2	E87401	adenine specific D
590	6	1.7	312	2	G69204	fructose-bisphosph	663	1.7	347	2	T08462	butyrolactone auto
591	6	1.7	313	2	E40590	ribose-phosphate p	664	1.7	348	2	E90492	proline lminopepti
592	6	1.7	314	2	F71076	motA homolog laft	665	1.7	349	2	F90296	hypothetical prote
593	6	1.7	315	2	S72843	hypothetical prote	666	1.7	350	2	T35646	hypothetical prote
594	6	1.7	316	2	S07193	ATP phosphoribosyl	667	1.7	351	2	B97507	probable thiamin m
595	6	1.7	317	2	T51595	chorion protein s3	668	1.7	352	2	AE2725	transcription regu
596	6	1.7	318	2	JC5552	ATP-phosphoribosyl	669	1.7	353	2	H86765	L-lactate dehydrog
597	6	1.7	319	2	H87072	phosphate transpor	670	1.7	354	2	S25513	outer membrane pro
598	6	1.7	320	2	S30257	hypothetical 30.3k	671	1.7	355	2	S25514	outer membrane pro
599	6	1.7	321	2	S30257	ATP phosphoribosyl	672	1.7	356	2	S20032	hypothetical prote
600	6	1.7	322	2	S38806	phycocyanin linker	673	1.7	357	2	H75631	probable dipeptida
601	6	1.7	323	2	AE2006	porin opmA - Rhodo	674	1.7	358	2	A83174	iron ABC transport
602	6	1.7	324	2	T02543	hypothetical prote	675	1.7	359	2	A31607	probable transcript
603	6	1.7	325	2	F82938	aldehyde dehydroge	676	1.7	360	2	S20494	3-oxoacyl-[acyl-ca
604	6	1.7	326	2	T35270	iron(III) dicitrat	677	1.7	361	2	C97677	probable glycerol-
605	6	1.7	327	2	F97480	hypothetical alani	678	1.7	362	2	A12901	glycerol-3-phospha
606	6	1.7	328	2	S09209	probable dehydroge	679	1.7	363	2	A96619	crfA protein - Rho
607	6	1.7	329	2	H72378	chorion protein s3	680	1.7	364	2	T50744	spheroidene monoox
608	6	1.7	330	2	T46617	conserved hypothet	681	1.7	365	2	F90180	sun (fmu) protein
609	6	1.7	331	2	D70314	probable hypothet	682	1.7	366	2	F87318	transcription regu
610	6	1.7	332	2	S55063	heme O oxygenase -	683	1.7	367	2	F84786	probable farnesyla
611	6	1.7	333	2	C82787	conserved hypothet	684	1.7	368	2	E83084	rod shape-determin
612	6	1.7	334	2	F81325	hypothetical prote	685	1.7	369	2		
613	6	1.7	335	2	F97463	probable lysR-like	686	1.7	370	2		

687	1.7	330	2	S40853	probable 2-keto-3-	760	1.7	357	2	S20736	porin precursor -
688	1.7	330	2	C86080	2-keto-3-deoxy-D-g	761	1.7	358	2	T00578	probable GDSP-mot
689	1.7	330	2	C91233	2-keto-3-deoxy-D-g	762	1.7	359	2	B86409	F349.6 protein - A
690	1.7	331	2	B95914	conserved hypothet	763	1.7	360	2	SI7456	outer membrane pro
691	1.7	331	2	G90984	probable UDP-galac	764	1.7	360	2	G82994	glycine-cleavage s
692	1.7	331	2	B85830	probable UDP-galac	765	1.7	360	2	S60268	beta-mannosidase (
693	1.7	332	2	E70384	biotin synthase (E	766	1.7	360	2	D86200	protein F12K11.20
694	1.7	332	2	B82607	conserved hypothet	767	1.7	361	2	F69798	conserved hypothet
695	1.7	333	2	T23840	hypothetical prote	768	1.7	361	2	T16175	hypothetical prote
696	1.7	333	2	B36532	hypothetical prote	769	1.7	362	2	H69785	mannan endo-1,4-b
697	1.7	334	2	D71655	thioredoxin reduct	770	1.7	362	2	B83057	tRNA (uracil-5-)-m
698	1.7	335	2	D83842	biotin synthase [i	771	1.7	363	2	T28726	hypothetical prote
699	1.7	335	2	B90044	stage v sporulatio	772	1.7	363	2	H69831	acetyl-CoA C-acety
700	1.7	335	2	T33457	hypothetical prote	773	1.7	364	2	H87184	5'-phosphoribosyl-
701	1.7	335	2	T16330	hypothetical prote	774	1.7	364	2	D86253	hypothetical prote
702	1.7	336	2	JC4102	hypothetical 36.9k	775	1.7	364	2	T17584	probable beta-1,3-
703	1.7	337	1	DE2VG3	glyceraldehyde-3-p	776	1.7	365	2	E82052	tryptophanyl-tRNA
704	1.7	337	2	S36824	beta-galactoside a	777	1.7	365	2	E98133	GTP cyclohydrolase
705	1.7	339	2	D83201	probable glycosyl	778	1.7	366	2	C84931	hypothetical prote
706	1.7	339	2	JC7712	transcription coac	779	1.7	367	2	T54455	DNA-directed DNA p
707	1.7	340	2	I54229	beta-galactoside a	780	1.7	367	2	G69316	auxin transport pr
708	1.7	340	2	T20807	hypothetical prote	781	1.7	368	2	S74983	hypothetical prote
709	1.7	341	2	AD3252	uroporphyrinogen d	782	1.7	369	2	A72453	cell division prot
710	1.7	341	2	A12760	DNA polymerase III	783	1.7	369	2	T51695	hypothetical prote
711	1.7	342	2	E96668	protein F1N19.3 [i	784	1.7	371	2	AF2314	hypothetical prote
712	1.7	342	2	AD3252	Gal beta 1,3GalNAc	785	1.7	371	2	AF2314	hypothetical prote
713	1.7	343	2	T02399	hypothetical prote	786	1.7	371	2	F70555	hypothetical prote
714	1.7	343	2	B72507	hypothetical prote	787	1.7	371	2	T21153	hypothetical prote
715	1.7	345	1	VABPA7	major capsid prote	788	1.7	371	2	G96937	cell wall-associat
716	1.7	345	2	B75274	conserved hypothet	789	1.7	373	2	JC7087	hypothetical prote
717	1.7	346	2	S72475	glucanase (EC 3.2.	790	1.7	373	2	H97108	hypothetical prote
718	1.7	346	2	AB2260	glucanase (importe	791	1.7	373	2	S43455	ft32 protein - Ach
719	1.7	347	2	E72065	sulfite reductase	792	1.7	373	2	S43455	cell division GRPa
720	1.7	347	2	A43815	transforming prote	793	1.7	374	2	A96502	hypothetical prote
721	1.7	347	2	G83171	hypothetical prote	794	1.7	374	2	F86243	probable acyl-acyl
722	1.7	347	2	H86558	sulfite reductase	795	1.7	374	2	T33844	ZIP4, probable zin
723	1.7	349	2	I39535	probable L-lactate	796	1.7	375	2	C71917	hypothetical prote
724	1.7	349	2	S57538	END3 protein - yea	797	1.7	375	2	T03325	probable transamin
725	1.7	349	2	D98170	sugar ABC transpor	798	1.7	375	2	T33778	gene i18 protein -
726	1.7	350	2	JC7188	REIC protein - hum	799	1.7	375	2	F88947	hypothetical prote
727	1.7	350	2	F97169	sialic acid syntha	800	1.7	376	2	C69813	protein C39F7.2 [i
728	1.7	350	2	E71373	probable regulator	801	1.7	376	2	D84577	RNA helicase homol
729	1.7	350	2	G97541	DNA polymerase II	802	1.7	376	2	D84577	probable reca prot
730	1.7	351	2	T29369	hypothetical prote	803	1.7	376	2	T40591	O-demethylpuromyci
731	1.7	352	2	A32780	photosystem II pro	804	1.7	376	2	T29270	hypothetical prote
732	1.7	352	2	A85531	hypothetical prote	805	1.7	376	2	D87700	hypothetical prote
733	1.7	352	2	E90680	probable ABC trans	806	1.7	377	2	E87022	iron-sulfur-bindin
734	1.7	353	1	FMSP32	photosystem II pro	807	1.7	377	2	B27718	probable conserved
735	1.7	353	1	FMN3D	photosystem II pro	808	1.7	378	2	F95844	cytochrome P450 2C
736	1.7	353	1	FMH32	photosystem II pro	809	1.7	378	2	S41869	probable dihydroli
737	1.7	353	1	FMSX3N	photosystem II pro	810	1.7	378	2	S41870	surface antigen -
738	1.7	353	1	FMN32	photosystem II pro	811	1.7	378	2	T35403	probable polypheny
739	1.7	353	1	FMSX32	photosystem II pro	812	1.7	378	2	F84230	RNA 3'-terminal ph
740	1.7	353	1	FMN232	photosystem II pro	813	1.7	378	2	T06512	DNA-binding protei
741	1.7	353	1	F2VFD1	photosystem II pro	814	1.7	379	2	T09943	conserved hypothet
742	1.7	353	1	F2DWD1	photosystem II pro	815	1.7	379	2	AE3003	probable 12-oxophy
743	1.7	353	1	F2CN1U	photosystem II pro	816	1.7	380	2	S62742	conserved hypothet
744	1.7	353	1	F2PMD1	photosystem II pro	817	1.7	380	2	S62743	endopolygalacturon
745	1.7	353	1	F2PMD1	photosystem II pro	818	1.7	380	2	T04284	endopolygalacturon
746	1.7	353	1	F2PMD1	photosystem II pro	819	1.7	381	2	S38824	hypothetical prote
747	1.7	353	1	F2PMD1	photosystem II pro	820	1.7	382	2	A72634	hypothetical prote
748	1.7	353	1	F2PMD1	photosystem II pro	821	1.7	382	2	T09600	cellular tumor ant
749	1.7	353	2	A25579	photosystem II pro	822	1.7	382	2	T14336	hypothetical prote
750	1.7	353	2	A25580	photosystem II pro	823	1.7	383	1	CEEC2	catechol O-methyl
751	1.7	353	2	S33912	photosystem II pro	824	1.7	383	1	C90641	RAD23 protein, iso
752	1.7	353	2	S57265	photosystem II pro	825	1.7	383	2	C90641	cell division prot
753	1.7	353	2	S42492	photosystem II pro	826	1.7	383	2	AE0069	cell division prot
754	1.7	353	2	H83482	photosystem II pro	827	1.7	383	2	C85492	cell division prot
755	1.7	354	1	S18595	hypothetical prote	828	1.7	383	2	AB0519	hypothetical prote
756	1.7	354	2	T48649	glycerol-3-phospha	829	1.7	383	2	T21583	hypothetical prote
757	1.7	355	2	S41285	coat protein - swe	830	1.7	384	2	T21946	hypothetical prote
758	1.7	355	2	D48376	poly(3-hydroxyvalk	831	1.7	384	2	A84955	cell division prot
759	1.7	355	2	S29274	poly (3-hydroxybut	832	1.7	384	2	H64505	hypothetical prote
					hypothetical prote					D69548	conserved hypothet

833	6	1.7	385	2	T22678	hypothetical prote	906	1.7	410	2	C86835	hypothetical prote
834	6	1.7	385	2	E83491	probable membrane-	907	1.7	411	2	S35333	steroid receptor p
835	6	1.7	386	2	S74778	hypothetical prote	908	1.7	411	2	A70509	hypothetical prote
836	6	1.7	386	2	B75616	conserved hypothet	909	1.7	411	2	T51818	ATP phosphoribosyl
837	6	1.7	386	2	F83994	xylose operon tran	910	1.7	411	2	D71803	ubiquinol-cytochro
838	6	1.7	388	2	S34672	alkaline serine pr	911	1.7	412	2	C64712	ubiquinol-cytochro
839	6	1.7	388	2	S76932	probable phosphori	912	1.7	413	2	B82760	cell division prot
840	6	1.7	389	1	SAVLAH	large-surface anti	913	1.7	413	2	S60930	probable membrane
841	6	1.7	389	1	SAVLBH	large-surface anti	914	1.7	413	2	A62905	sensory transducti
842	6	1.7	389	1	SAVLBJ	large-surface anti	915	1.7	413	2	AH2743	conserved hypothet
843	6	1.7	389	1	SAVLAI	large-surface anti	916	1.7	413	2	G69333	probable acyl-CoA
844	6	1.7	389	1	SAVLCP	large-surface anti	917	1.7	414	2	S34829	triase phosphate/3
845	6	1.7	389	2	S41871	large-surface anti	918	1.7	414	2	S23224	triase phosphate/3
846	6	1.7	389	2	S47407	surface antigen -	919	1.7	414	2	A37133	apolipoprotein A-I
847	6	1.7	389	2	S32202	surface antigen -	920	1.7	414	2	I48975	hypothetical prote
848	6	1.7	389	2	S20715	large surface anti	921	1.7	414	2	T22498	hypothetical prote
849	6	1.7	389	2	S20749	surface antigen -	922	1.7	415	2	T19099	hypothetical prote
850	6	1.7	389	2	S20753	surface antigen -	923	1.7	415	2	G64542	glycine hydroxymet
851	6	1.7	389	2	B75363	glutamate N-acetyl	924	1.7	416	2	G71965	hypothetical prote
852	6	1.7	389	2	B96635	hypothetical prote	925	1.7	416	2	G97524	hypothetical prote
853	6	1.7	389	2	I49640	transcription fact	926	1.7	416	2	G69250	hypothetical prote
854	6	1.7	389	2	G70120	outer membrane pro	927	1.7	418	2	T15142	hypothetical prote
855	6	1.7	389	2	F75411	conserved hypothet	928	1.7	419	2	T15088	hypothetical prote
856	6	1.7	390	1	DNWS53	cellular tumor ant	929	1.7	419	2	A57000	orphan receptor CO
857	6	1.7	390	2	T04097	cell division prot	930	1.7	420	2	T36272	phosphoglycerate k
858	6	1.7	390	2	S58814	acyl-[acyl-carrier	931	1.7	420	2	TVUTG4	probable glutamate
859	6	1.7	390	2	A98336	cystathionine gamm	932	1.7	420	2	A81895	envelope protein -
860	6	1.7	390	2	A12946	methionine gamma-1	933	1.7	420	2	T42616	hypothetical prote
861	6	1.7	390	2	JS0296	transposase - Staph	934	1.7	420	2	H84890	hypothetical prote
862	6	1.7	390	2	S44285	EAR2 protein - mou	935	1.7	420	2	T36072	hypothetical prote
863	6	1.7	391	2	C84268	aspartate aminotra	936	1.7	421	2	KTUTGC	hypothetical prote
864	6	1.7	391	2	T34935	hypothetical prote	937	1.7	421	2	I64185	phosphoglycerate k
865	6	1.7	393	1	DNHU53	cellular tumor ant	938	1.7	421	2	T25205	gene II protein -
866	6	1.7	393	1	S06594	cellular tumor ant	939	1.7	421	2	T32BP1K	citrate synthase-1
867	6	1.7	393	2	T07653	acyl-[acyl-carrier	940	1.7	421	2	A43393	bicyclomycin resis
868	6	1.7	393	2	C83155	probable MFS trans	941	1.7	421	2	H70607	hypothetical prote
869	6	1.7	394	2	T51494	stearyl-acyl carr	942	1.7	422	2	JC5524	26S proteasome reg
870	6	1.7	395	2	AD2119	hypothetical prote	943	1.7	422	2	T47901	endosperm specific
871	6	1.7	395	2	T48301	protein kinase-lik	944	1.7	422	2	I48305	gene COUP-TF1 prot
872	6	1.7	395	2	F82852	conserved hypothet	945	1.7	422	2	T06774	cell division prot
873	6	1.7	396	2	B39170	acyl-[acyl-carrier	946	1.7	423	2	S02710	transcription fact
874	6	1.7	396	2	S31959	acyl-[acyl-carrier	947	1.7	423	2	D95565	F6D8-29 [Imported]
875	6	1.7	396	2	A91019	probable antibiotti	948	1.7	423	2	T45317	probable 26S prote
876	6	1.7	396	2	C85863	probable antibiotti	949	1.7	424	2	I40646	sensor-like protei
877	6	1.7	397	2	S20617	transcription fact	950	1.7	424	2	T38548	hypothetical zinc-
878	6	1.7	398	1	VBBPA7	minor capsid prote	951	1.7	425	2	T18723	probable transfera
879	6	1.7	398	2	S23351	hypothetical 43.3	952	1.7	425	2	H70390	conserved hypothet
880	6	1.7	398	2	A64982	probable outer mem	953	1.7	426	2	C96676	hypothetical prote
881	6	1.7	398	2	B85851	acyl-[acyl-carrier	954	1.7	426	2	T50593	probable membrane
882	6	1.7	399	2	OHSPAD	large-surface anti	955	1.7	428	2	AD2939	hypothetical prote
883	6	1.7	399	2	S24995	acyl-[acyl-carrier	956	1.7	429	2	T21060	hypothetical prote
884	6	1.7	400	1	SAVLA	large-surface anti	957	1.7	430	2	T36682	probable secreted
885	6	1.7	401	1	A36961	pilin biogenesis p	958	1.7	431	2	F83123	probable ABC tran
886	6	1.7	401	2	E84869	histidine-TRNA lig	959	1.7	431	2	B87285	phosphate porin PA4
887	6	1.7	401	2	S76788	phosphate transloc	960	1.7	432	2	E87508	probable membrane
888	6	1.7	401	2	S42583	hypothetical prote	961	1.7	432	2	D65132	histidinol dehydro
889	6	1.7	401	2	H83911	hypothetical prote	962	1.7	432	2	H90162	hypothetical prote
890	6	1.7	402	2	AD1417	drug-efflux transp	963	1.7	432	2	S20060	translation elonga
891	6	1.7	402	2	AD1792	procollagen I C-pr	964	1.7	433	2	A10536	translation elonga
892	6	1.7	402	2	JH0403	TcAB protein [impo	965	1.7	434	2	DEECHT	translation elonga
893	6	1.7	402	2	F90035	diacylphosphamide a	966	1.7	434	2	H86279	translation elonga
894	6	1.7	402	2	S73773	steroid receptor p	967	1.7	435	2	T46107	ubiquitin transalo
895	6	1.7	403	2	S35334	ear-2 protein - hu	968	1.7	436	2	C86823	ubiquitin carboxyl
896	6	1.7	403	2	S02709	hypothetical prote	969	1.7	436	2	A54595	sugar-binding prot
897	6	1.7	403	2	B70659	hypothetical prote	970	1.7	437	2	A70587	transcription fact
898	6	1.7	404	2	F59097	hypothetical prote	971	1.7	437	2	A70587	transcription fact
899	6	1.7	404	2	T71264	acyl-[acyl-carrier	972	1.7	438	1	S24085	preprotein translo
900	6	1.7	407	2	A47488	aminoacylase (EC 3	973	1.7	438	2	T39772	ubiquitin carboxyl
901	6	1.7	408	2	S71264	peptidase T (amino	974	1.7	438	2	C98343	sugar-binding prot
902	6	1.7	408	2	E66958	hypothetical prote	975	1.7	438	2	B72313	glutamine syntheta
903	6	1.7	409	2	T20847	hypothetical prote	976	1.7	439	2	S20489	S-locus-specific g
904	6	1.7	409	2	T18726	orphan receptor CO	977	1.7	439	2		
905	6	1.7	410	2	I50689		978	1.7	439	2		



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RESULT 2
162385
outer membrane protein ompA - Escherichia vulneris (fragment)
N:Alternate names: Outer membrane protein II
C:Species: Escherichia vulneris
C:Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 20-Aug-1999
C:Accession: I62385
R:Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A:Title: Molecular and evolutionary relationships among enteric bacteria.
A:Reference number: I40701; MUID:92065252; PMID:1955870
A:Accession: I62385
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-238 <RES>
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C:Genetics:

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Query Match          15.4%; Score 53; DB 2; Length 238;
Best Local Similarity 100.0%; Pred. NO. 8e-46;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 213 FTLLKSDVLFNFNKATLKPEGQQALDQLYTOLSNMDPKDSAVVLGYTDRI GSE 265
|||||
DB 116 FTLLKSDVLFNFNKATLKPEGQQALDQLYTOLSNMDPKDSAVVLGYTDRI GSE 168
|||||

RESULT 3
S07222
outer membrane protein ompA precursor - Enterobacter aerogenes
C:Species: Enterobacter aerogenes
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 20-Aug-1999
C:Accession: S07222

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Query Match	97.4%	Score 335;	DB 2;	Length 356;	
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Matches 335;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
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Db	21	AAPKDNWTYAGGKLGSQYHDTGYGNGFQNNNGPTRNDOLGAGAFGSGYQVNPYLGFGMG	80		
QY	69	YDWLGRMAYKGSVDNCAEFAQAGVOLTAKLGYPTDDLDIYTRLGGMWRAADSKGNVASTG	128		
Db	81	YDWLGRMAYKGSVDNCAEFAQAGVOLTAKLGYPTDDLDIYTRLGGMWRAADSKGNVASTG	140		
QY	129	VSSEHDTGVSVPFAGGVEMAVTROIATRLFYQVNNIGDAGTVGTRPDNGMLSLGVSYSR	188		
Db	141	VSSEHDTGVSVPFAGGVEMAVTROIATRLFYQVNNIGDAGTVGTRPDNGMLSLGVSYSR	200		
QY	189	FGQEDAAPVPAPAPAPAEVATKHFTLKSVDYLFNFENKATLKPGEQOALDQLYXTOLSNMDF	248		
Db	201	FGQEDAAPVPAPAPAPAEVATKHFTLKSVDYLFNFENKATLKPGEQOALDQLYXTOLSNMDF	260		
QY	249	KDGSAVVLGYTRDIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNT	308		
Db	261	KDGSAVVLGYTRDIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNT	320		
QY	309	CDNVKARAALIDCIAPDRRVEIEVKGYEYVTOPA	343		

[illegible]

RESULT 4  
I40703  
Outer membrane protein A - Citrobacter freundii (fragment)  
N:Alternate names: Outer membrane protein II  
C:Species: Citrobacter freundii

C>Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 20-Aug-1999  
 C:Accession: I40703  
 R:Lawrence, J.G.; Ochman, H.; Hartl, D.L.  
 J. Gen. Microbiol. 137, 1911-1921, 1991  
 A:Title: Molecular and evolutionary relationships among enteric bacteria.  
 A:Reference number: I40701; MUID:92065252; PMID:1955870  
 A:Accession: I40703  
 A:Status: preliminary; translated from GB/EMBL/DBSJ  
 A:Molecule type: DNA  
 A:Residues: 1-238 <RES>  
 A:Cross-references: GB:M63354; NID:g144441; PIDN:AA230395.1; PID:g144442  
 C:Genetics:  
 A:Gene: ompA  
 C:Superfamily: outer membrane protein A  
 C:Keywords: membrane protein  
 F:99-109/Region: alanine/proline-rich

Query Match 12.5%; Score 43; DB 2; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-35;  
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 KISARGMESNPVTGTCNVKARALDCLAPDRRVEIEVKG 334  
 |||||  
 DB 195 KISARGMESNPVTGTCNVKARALDCLAPDRRVEIEVKG 237

RESULT 5  
 MMECA  
 outer membrane protein A precursor - Escherichia coli (strain K-12)  
 C:Alternate names: outer membrane protein II\*  
 C:Species: Escherichia coli  
 C>Date: 30-Sep-1980 #sequence\_revision 30-Sep-1980 #text\_change 01-Mar-2002  
 C:Accession: A93707; A92862; A93855; S50909; D64836; A03434  
 R:Beck, E.; Bremer, E.  
 Nucleic Acids Res. 8, 3011-3024, 1980  
 A:Title: Nucleotide sequence of the gene ompA coding the outer membrane protein II of Escherichia coli.  
 A:Reference number: A93707; MUID:81053729; PMID:6253901  
 A:Accession: A93707  
 A:Molecule type: DNA  
 A:Residues: 1-346 <BSC>  
 A:Cross-references: GB:V00307; GB:J01654; NID:g42159; PIDN:CAA23588.1; PID:g42161  
 A:Experimental source: strain K12  
 R:Govva, N.R.; Nakamura, K.; Inouye, M.  
 J. Mol. Biol. 143, 317-328, 1980  
 A:Title: Gene structure of the OmpA protein, a major surface protein of Escherichia coli.  
 A:Reference number: A92862; MUID:81170587; PMID:6260961  
 A:Accession: A92862  
 A:Molecule type: DNA  
 A:Residues: 1-346 <MOV>  
 A:Cross-references: GB:J01654; GB:V00307; GB:V00358; NID:g46979; PIDN:AAA24231.1; PID:g46979  
 A:Experimental source: K12, strain K802  
 R:Chen, R.; Schmidmayr, W.; Kramer, C.; Chen-Schmeisser, U.; Henning, U.  
 Proc. Natl. Acad. Sci. U.S.A. 77, 4592-4596, 1980  
 A:Title: Primary structure of major outer membrane protein II\* (ompA protein) of Escherichia coli.  
 A:Reference number: A93855; MUID:81054820; PMID:7001461  
 A:Accession: A93855  
 A:Molecule type: protein  
 A:Residues: 23-346 <CHE>  
 A:Experimental source: K12, strain P400  
 R:Kuhn, A.; Kleifer, D.; Koehne, C.; Zhu, H.X.; Tschantz, W.R.; Dalbey, R.E.  
 Eur. J. Biochem. 226, 891-897, 1994  
 A:Title: Evidence for a loop-like insertion mechanism of pro-Omp A into the inner membrane.  
 A:Reference number: S50909; MUID:95112855; PMID:7813480  
 A:Accession: S50909  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-46 <KUH>  
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shao, Y.  
 Science 277, 1453-1462, 1997  
 A:Title: The complete genome sequence of Escherichia coli K-12.  
 A:Reference number: A64720; MUID:97426617; PMID:9278503  
 A:Accession: D64836

A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-346 <BLAT>  
 A:Cross-references: GB:AE000198; GB:U00096; NID:g1787189; PIDN:AA274043.1; PID:g17871  
 A:Experimental source: strain K-12, substrain MG1655  
 C:Genetics:  
 A:Gene: ompA; tolG; tut; con  
 A:Map position: 22 min  
 C:Function:  
 A:Description: required for the action of colicins K and L and for the stabilization of diffusion channels that allow penetration of various solutes  
 C:Superfamily: outer membrane protein A  
 C:Keywords: membrane protein; monomer  
 F:1-21/Domain: signal sequence #status predicted <SIG>  
 F:22-346/Product: outer membrane protein A #status predicted <MAT>  
 F:22-196/Domain: intramembrane #status predicted <INT>  
 F:196-208/Region: alanine/proline-rich  
 F:209-346/Domain: periplasmic #status predicted <PER>  
 F:257-301/Domain: ompA-like domain #status predicted <OMP>

Query Match 9.6%; Score 33; DB 1; Length 346;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-25;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 KAQGVQLTAKLGYPTITDLDIYTRLGGMVWRAD 119  
 |||||  
 DB 94 KAQGVQLTAKLGYPTITDLDIYTRLGGMVWRAD 126

## RESULT 6

A90759

outer membrane protein 3a ECs1041 [imported] - Escherichia coli (strain O157:H7, substrain O157:H7)  
 C:Species: Escherichia coli  
 C>Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 01-Mar-2002  
 C:Accession: A90759  
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.; gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
 DNA Res. 8, 11-22, 2001  
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and 94  
 A:Reference number: A99629; MUID:21156231; PMID:11258796  
 A:Accession: A90759  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-346 <HAY>  
 A:Cross-references: GB:BA000007; PIDN:BA834464.1; PID:g13360501; GSPDB:GN00154  
 A:Experimental source: strain O157:H7, substrain RMD 050952  
 C:Genetics:  
 A:Gene: ECs1041  
 C:Superfamily: outer membrane protein A

Query Match 9.6%; Score 33; DB 2; Length 346;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-25;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 KAQGVQLTAKLGYPTITDLDIYTRLGGMVWRAD 119  
 |||||  
 DB 94 KAQGVQLTAKLGYPTITDLDIYTRLGGMVWRAD 126

## RESULT 7

G85622

outer membrane protein 3a [imported] - Escherichia coli (strain O157:H7, substrain EC O157:H7)  
 C:Species: Escherichia coli  
 C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 01-Mar-2002  
 C:Accession: G85622  
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May, A.; Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda, Nature 409, 529-533, 2001  
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
 A:Reference number: A85480; MUID:21074935; PMID:11206551  
 A:Accession: G85622  
 A:Status: preliminary  
 A:Molecule type: DNA

A:Residues: 1-346 <STO>  
A:Cross-references: GB:AE005174; NID:gl2514142; PIDN:AA655443.1; GSPDB:GN00145; UWGP:213  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: ompA  
C:Superfamily: outer membrane protein A

Query Match 9.6%; Score 33; DB 2; Length 346;  
Best Local Similarity 100.0%; Pred. No. 2.6e-25;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 KAQGVQLTAKLGYPIITDDLDIYTRLGGMVVRAD 119  
|||||  
Db 94 KAQGVQLTAKLGYPIITDDLDIYTRLGGMVVRAD 126

RESULT 8  
I62386  
outer membrane protein A - Escherichia hermannii (fragment)  
N:Alternate names: outer membrane protein II  
C:Species: Escherichia hermannii  
C:Date: 04-Sep-1997 #sequence\_revision 07-Nov-1997 #text\_change 04-Mar-2000  
C:Accession: I62386; I62390  
R:Lawrence, J.G.; Ochman, H.; Hartl, D.L.  
J. Gen. Microbiol. 137, 1911-1921, 1991  
A:Title: Molecular and evolutionary relationships among enteric bacteria.  
A:Reference number: I40701; MUID:92065252; PMID:1955870  
A:Accession: I62386  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-243 <RES>  
A:Cross-references: GB:M63346; NID:gl146986; PIDN:AAA24234.1; PID:gl146987  
A:Accession: I62390  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-243 <RES>  
A:Cross-references: GB:M63347; NID:gl146994; PIDN:AAA24238.1; PID:gl146995  
A:Experimental source: ATCC 33652  
C:Genetics:  
A:Gene: ompA  
C:Superfamily: outer membrane protein A  
C:Keywords: membrane protein  
F:103-114/Region: alanine/proline-rich

Query Match 8.4%; Score 29; DB 2; Length 243;  
Best Local Similarity 100.0%; Pred. No. 2.3e-21;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 210 TKHFTLKSVDLFNFNFKATLKPEGQQALDQ 238  
|||||  
Db 118 TKHFTLKSVDLFNFNFKATLKPEGQQALDQ 146

RESULT 9  
I62389  
outer membrane protein ompA - Escherichia vulneris (ATCC 33821) (fragment)  
N:Alternate names: outer membrane protein II  
C:Species: Escherichia vulneris  
A:Variety: ATCC 33821  
C:Date: 04-Sep-1997 #sequence\_revision 07-Nov-1997 #text\_change 20-Aug-1999  
C:Accession: I62389  
R:Lawrence, J.G.; Ochman, H.; Hartl, D.L.  
J. Gen. Microbiol. 137, 1911-1921, 1991  
A:Title: Molecular and evolutionary relationships among enteric bacteria.  
A:Reference number: I40701; MUID:92065252; PMID:1955870  
A:Accession: I62389  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-244 <RES>  
A:Cross-references: GB:M63349; NID:gl146992; PIDN:AAA24237.1; PID:gl146993  
A:Experimental source: ATCC 33821  
C:Genetics:  
A:Gene: ompA

C:Superfamily: outer membrane protein A  
C:Keywords: membrane protein  
F:104-115/Region: alanine/proline-rich

Query Match 8.4%; Score 29; DB 2; Length 244;  
Best Local Similarity 100.0%; Pred. No. 2.3e-21;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 210 TKHFTLKSVDLFNFNFKATLKPEGQQALDQ 238  
|||||  
Db 119 TKHFTLKSVDLFNFNFKATLKPEGQQALDQ 147

RESULT 10  
I62393  
outer membrane protein ompA - Escherichia vulneris (ATCC 33822) (fragment)  
N:Alternate names: outer membrane protein II  
C:Species: Escherichia vulneris  
A:Variety: ATCC 33822  
C:Date: 04-Sep-1997 #sequence\_revision 07-Nov-1997 #text\_change 20-Aug-1999  
C:Accession: I62393  
R:Lawrence, J.G.; Ochman, H.; Hartl, D.L.  
J. Gen. Microbiol. 137, 1911-1921, 1991  
A:Title: Molecular and evolutionary relationships among enteric bacteria.  
A:Reference number: I40701; MUID:92065252; PMID:1955870  
A:Accession: I62393  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-244 <RES>  
A:Cross-references: GB:M63350; NID:gl147000; PIDN:AAA24241.1; PID:gl147001  
A:Experimental source: ATCC 33822  
C:Genetics:  
A:Gene: ompA  
C:Superfamily: outer membrane protein A  
C:Keywords: membrane protein  
F:104-115/Region: alanine/proline-rich

Query Match 8.4%; Score 29; DB 2; Length 244;  
Best Local Similarity 100.0%; Pred. No. 2.3e-21;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 210 TKHFTLKSVDLFNFNFKATLKPEGQQALDQ 238  
|||||  
Db 119 TKHFTLKSVDLFNFNFKATLKPEGQQALDQ 147

RESULT 11  
I84531  
outer membrane protein A - Escherichia fergusonii (ATCC 35469) (fragment)  
N:Alternate names: outer membrane protein II  
C:Species: Escherichia fergusonii  
A:Variety: ATCC 35469  
C:Date: 04-Sep-1997 #sequence\_revision 07-Nov-1997 #text\_change 20-Aug-1999  
C:Accession: I84531  
R:Lawrence, J.G.; Ochman, H.; Hartl, D.L.  
J. Gen. Microbiol. 137, 1911-1921, 1991  
A:Title: Molecular and evolutionary relationships among enteric bacteria.  
A:Reference number: I40701; MUID:92065252; PMID:1955870  
A:Accession: I84531  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-243 <RES>  
A:Cross-references: GB:M63351; NID:gl146982; PIDN:AAA24232.1; PID:gl146983  
A:Experimental source: ATCC 35469  
C:Genetics:  
A:Gene: ompA  
C:Superfamily: outer membrane protein A  
C:Keywords: membrane protein  
F:103-114/Region: alanine/proline-rich

Query Match 7.8%; Score 27; DB 2; Length 243;  
Best Local Similarity 100.0%; Pred. No. 2.5e-19;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 LTKALGYPITDDLDIYTRLGGMWRAD 119  
|||||  
Db 1 LTKALGYPITDDLDIYTRLGGMWRAD 27

## RESULT 12

MMEBAT

outer membrane protein A - Escherichia fergusonii (ATCC 35472) (fragment)  
N:Alternate names: outer membrane protein II  
C:Species: Escherichia fergusonii  
A:Variety: ATCC 35472  
C:Date: 04-Sep-1997 #sequence\_revision 07-Nov-1997 #text\_change 04-Mar-2000  
C:Accession: I62388; I62392  
R:Lawrence, J.G.; Ochman, H.; Hartl, D.L.  
J. Gen. Microbiol. 137, 1911-1921, 1991  
A:Title: Molecular and evolutionary relationships among enteric bacteria.  
A:Reference number: I40701; MUID:92065252; PMID:1955870  
A:Accession: I62388  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-243 <RES>  
A:Cross-references: GB:M63352; NID:gl46990; PIDN:AAA24236.1; PID:gl46991  
A:Experimental source: ATCC 35471  
A:Accession: I62392  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-243 <RE2>  
A:Cross-references: GB:M63353; NID:gl46998; PIDN:AAA24240.1; PID:gl46999  
A:Experimental source: ATCC 35472  
C:Genetics:  
A:Gene: ompA  
C:Superfamily: outer membrane protein A  
C:Keywords: membrane protein  
F:103-114/Region: alanine/proline-rich

Query Match 7.8%; Score 27; DB 2; Length 243;  
Best Local Similarity 100.0%; Pred. No. 2.5e-19;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 LTKALGYPITDDLDIYTRLGGMWRAD 119  
|||||  
Db 1 LTKALGYPITDDLDIYTRLGGMWRAD 27

## RESULT 13

MMEBAT

outer membrane protein A precursor - Shigella dysenteriae  
C:Species: Shigella dysenteriae  
C:Date: 18-Aug-1982 #sequence\_revision 18-Aug-1982 #text\_change 16-Jul-1999  
C:Accession: A03435  
R:Braun, G.; Cole, S.T.  
Nucleic Acids Res. 10, 2367-2378, 1982  
A:Title: The nucleotide sequence coding for major outer membrane protein OmpA of Shigella  
A:Reference number: A03435; MUID:82221414; PMID:6283478  
A:Accession: A03435  
A:Molecule type: DNA  
A:Residues: 1-351 <BRA>  
A:Cross-references: GB:V01344; NID:g46943; PIDN:CAA24638.1; PID:g46945  
C:Genetics:  
A:Gene: ompA  
C:Superfamily: outer membrane protein A  
C:Keywords: transmembrane protein  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-351/Product: outer membrane protein A #status predicted <MAT>  
F:22-201/Domain: intramembrane #status predicted <INT>  
F:201-213/Region: alanine/proline-rich  
F:214-351/Domain: periplasmic #status predicted <PER>

Query Match 7.0%; Score 24; DB 1; Length 351;  
Best Local Similarity 100.0%; Pred. No. 3.8e-16;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 210 TKHFTLKSVDLNFENKATLKPEQG 233  
|||||  
Db 217 TKHFTLKSVDLNFENKATLKPEQG 240

## RESULT 14

MMEBAT

outer membrane protein A precursor - Salmonella typhimurium  
N:Alternate names: outer membrane major heat-modifiable protein; outer membrane prote  
C:Species: Salmonella typhimurium  
C:Date: 19-Feb-1984 #sequence\_revision 19-Feb-1984 #text\_change 16-Jul-1999  
C:Accession: A03436  
R:Freudl, R.; Cole, S.T.  
Eur. J. Biochem. 134, 497-502, 1983  
A:Title: Cloning and molecular characterization of the ompA gene from Salmonella typh  
A:Reference number: A03436; MUID:83287368; PMID:6349993  
A:Accession: A03436  
A:Molecule type: DNA  
A:Residues: 1-350 <PRE>  
A:Cross-references: GB:X02006; NID:g47798; PIDN:CAA26037.1; PID:g758341  
C:Genetics:  
A:Gene: ompA  
A:Map position: 20 min  
C:Function:  
A:Description: required for the action of colicins and for the stabilization of mat  
A:Note: cannot serve as the receptor for the ompA-specific phages K3 and TuII  
C:Superfamily: outer membrane protein A  
C:Keywords: transmembrane protein  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-350/Product: outer membrane protein A #status predicted <MAT>  
F:22-200/Domain: intramembrane #status predicted <INT>  
F:200-212/Region: alanine/proline-rich  
F:213-350/Domain: periplasmic #status predicted <PER>

Query Match 6.4%; Score 22; DB 1; Length 350;  
Best Local Similarity 100.0%; Pred. No. 4.2e-14;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 KISARGMGESNPVTGNTCDNVK 313  
|||||  
Db 298 KISARGMGESNPVTGNTCDNVK 319

## RESULT 15

A10626

outer membrane protein A STY1091 [Imported] - Salmonella enterica subsp. enterica ser  
C:Species: Salmonella enterica subsp. enterica serovar Typhi  
A:Note: this species has also been called Salmonella typhi  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 01-Mar-2002  
C:Accession: A10626  
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church  
th, T.; Conington, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr  
S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,  
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se  
A:Reference number: AB0502; PMID:11677608  
A:Accession: A10626  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-350 <PAR>  
A:Cross-references: GB:AL513382; PIDN:CAD08196.1; PID:gl6502245; GSPDB:GN00176  
C:Genetics:  
A:Gene: STY1091  
C:Superfamily: outer membrane protein A

Query Match 6.4%; Score 22; DB 2; Length 350;  
Best Local Similarity 100.0%; Pred. No. 4.2e-14;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 KISARGMGESNPVTGNTCDNVK 313  
|||||  
Db 298 KISARGMGESNPVTGNTCDNVK 319

Tue Apr 15 09:25:25 2003

us-09-831-061-2.oligo.rpr

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Search completed: April 15, 2003, 08:56:51  
Job time : 53 secs

GenCore version 5.1.4\_p5-4578  
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OM protein - protein search, using sw model

Run on: April 15, 2003, 08:49:29 ; Search time 14 Seconds  
(without alignments)  
1019.133 Million cell updates/sec

Title: US-09-831-061-2

Perfect score: 344

Sequence: 1 MKAFVNLNAPKNTWYAGG.....DRRVEIEVKYKEVVTQAG 344

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 5

Total number of hits satisfying chosen parameters: 8372

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	342	99.4	344	1	OMPA_KLEPN
2	53	15.4	350	1	OMPA_ENTAE
3	43	12.5	338	1	OMPA_CITFR
4	33	9.6	346	1	OMPA_ECOLI
5	29	8.4	243	1	OMPA_ESCHE
6	27	7.8	243	1	OMPA_ESCHE
7	24	7.0	351	1	OMPA_SHIDY
8	22	6.4	350	1	OMPA_SALTY
9	20	5.8	241	1	OMPA_ESCBL
10	19	5.5	359	1	OMPA_SERMA
11	17	4.9	243	1	OMPA_SPROD
12	12	3.5	349	1	OMPA_BUCAT
13	10	2.9	353	1	OM52_HAEIN
14	10	2.9	359	1	OM53_HAEIN
15	9	2.6	186	1	MLEI_MUGCA
16	9	2.6	192	1	MLEF_RAT
17	9	2.6	196	1	MLEF_HUMAN
18	9	2.6	383	1	NRL1_RHOR
19	9	2.6	458	1	ARLY_VIBCH
20	9	2.6	1061	1	RNE_ECOLI
21	9	2.6	1576	1	YLK3_CAEEL
22	9	2.6	3866	1	HRX_MOUSE
23	8	2.3	28	1	OMPA_YERPS
24	8	2.3	51	1	LB2_TETH
25	8	2.3	94	1	YB3H_ECOLI
26	8	2.3	187	1	MLEI_MOUSE
27	8	2.3	188	1	MLEI_RAT
28	8	2.3	190	1	MLEI_CHICK
29	8	2.3	191	1	MLEI_HUMAN
30	8	2.3	193	1	MLEI_RABIT
31	8	2.3	252	1	CRBL_BOVIN
32	8	2.3	260	1	HIL_VOLCA
33	8	2.3	313	1	EBAG_STRPL
34	8	2.3	316	1	CDNC_HUMAN
35	8	2.3	344	1	YH3A_YEAST
36	8	2.3	346	1	RA_HUMAN
37	8	2.3	353	1	OM51_HAEIN
38	8	2.3	355	1	FKB8_HUMAN
39	8	2.3	355	1	FKB8_MOUSE
40	8	2.3	423	1	CCG8_MOUSE
41	8	2.3	426	1	ASD4_NEUCR
42	8	2.3	437	1	BF1H_XENLA
43	8	2.3	439	1	XP2_XENLA
44	8	2.3	498	1	DGT1_MOUSE
45	8	2.3	498	1	DGT1_RAT
46	8	2.3	524	1	P60_LISWE
47	8	2.3	547	1	SPAK_HUMAN
48	8	2.3	551	1	TF65_HUMAN
49	8	2.3	553	1	ODP2_ALCEU
50	8	2.3	553	1	SPAK_RAT
51	8	2.3	556	1	SPAK_MOUSE
52	8	2.3	595	1	DCOA_KLEPN
53	8	2.3	603	1	NMBL_MOUSE
54	8	2.3	609	1	NMBL_HUMAN
55	8	2.3	622	1	3BPI_HUMAN
56	8	2.3	642	1	MB11_ARATH
57	8	2.3	676	1	ICPO_HSVBJ
58	8	2.3	676	1	ICPO_HSVBK
59	8	2.3	803	1	2XDB_HUMAN
60	8	2.3	806	1	MK07_MOUSE
61	8	2.3	1051	1	TEFA_MOUSE
62	8	2.3	1300	1	SAL3_HUMAN
63	8	2.3	1385	1	CTAL_MOUSE
64	8	2.3	2774	1	MAPA_RAT
65	7	2.0	14	1	LPW_ECOLI
66	7	2.0	66	1	Y7KD_STRLI
67	7	2.0	96	1	SY20_HUMAN
68	7	2.0	105	1	Y756_RICPR
69	7	2.0	133	1	NL21_PARJU
70	7	2.0	138	1	NL13_PARJU
71	7	2.0	155	1	BCCP_HAEIN
72	7	2.0	157	1	HES2_MOUSE
73	7	2.0	173	1	HES2_HUMAN
74	7	2.0	208	1	SPC3_STRPU
75	7	2.0	212	1	IF3_DSTRU
76	7	2.0	238	1	MNBA_WAIZE
77	7	2.0	243	1	RS3_SYN6
78	7	2.0	247	1	FMT_VIBAL
79	7	2.0	256	1	Y107_NPVOP
80	7	2.0	288	1	KLFD_HUMAN
81	7	2.0	289	1	KLFD_MOUSE
82	7	2.0	289	1	YFK2_YEAST
83	7	2.0	310	1	PR28_MYCTU
84	7	2.0	317	1	RSP4_URECA
85	7	2.0	325	1	MODD_MYCBO
86	7	2.0	325	1	MODD_MYCTU
87	7	2.0	329	1	TAL_MOUSE
88	7	2.0	331	1	TAL_HUMAN
89	7	2.0	337	1	NCA3_YEAST
90	7	2.0	345	1	CEBB_HUMAN
91	7	2.0	349	1	SCA3_MOUSE
92	7	2.0	351	1	VP39_NPVOP
93	7	2.0	354	1	PROW_SALTY
94	7	2.0	362	1	KLFL_HUMAN
95	7	2.0	370	1	KIT_FSVH2
96	7	2.0	379	1	AMPI_SCHPO
97	7	2.0	416	1	MTPI_PSVTA
98	7	2.0	457	1	ARLY_ECOS7
99	7	2.0	457	1	ARLY_ECOLI
100	7	2.0	457	1	ARLY_PASNU
101	7	2.0	457	1	ARLY_FERPE
102	7	2.0	457	1	V51K_ACLSA
103	7	2.0	458	1	ARLY_SALTY
104	7	2.0	458	1	ARLY_SALTY
105	7	2.0	473	1	BIAR_CANFA
106	7	2.0	474	1	CBF5_SCHPO

P49918 homo sapien  
P38768 saccharomyc  
Q9y2v3 homo sapien  
P43840 haemophilus  
Q14318 homo sapien  
Q35465 mus musculus  
Q8vhw2 mus musculus  
Q9hev5 neustopora  
P13735 xenopus lae  
P17437 xenopus lae  
Q922a7 mus musculus  
Q92m3 rattus norv  
Q01839 listeria we  
Q9uew8 homo sapien  
Q04206 homo sapien  
Q59098 alcaligenes  
Q88506 rattus norv  
Q921w9 mus musculus  
P13187 klebsiella  
Q08919 mus musculus  
Q9y0r0 homo sapien  
Q9y3l3 homo sapien  
Q9sav1 arabidopsis  
P29128 bovine herp  
P29836 bovine herp  
P98169 homo sapien  
Q9vhw8 mus musculus  
Q64127 mus musculus  
Q9bxa9 homo sapien  
Q54991 mus musculus  
P34926 rattus norv  
P30353 escherichia  
P22401 streptomyce  
P78556 homo sapien  
Q92c14 rickettsia  
P55958 parietaria  
Q40905 parietaria  
P43874 haemophilus  
Q54792 mus musculus  
Q9v543 homo sapien  
P18537 strongyloce  
Q9rsn7 deinococcus  
P38564 zea mays (m  
Q24695 synecococc  
Q87726 vibrio algi  
Q10346 orgyia psau  
Q942v9 h.kruappel-  
Q91jz6 mus musculus  
P43607 saccharomyc  
P71697 mycobacteri  
P38981 mycobacteri  
Q30620 mycobacteri  
Q50906 mycobacteri  
P22091 mus musculus  
P17542 homo sapien  
P46955 saccharomyc  
P17676 homo sapien  
Q35609 mus musculus  
P17500 orgyia psau  
P17327 salmonella  
Q13351 homo sapien  
P04048 feline sarc  
Q59730 schizosacch  
Q3481 psychrobact  
Q8x730 escherichia  
P11447 escherichia  
P57909 pasteurella  
Q8za88 yersinia pe  
P54892 apple chlor  
Q8z311 salmonella  
Q8zkl6 salmonella  
P79148 canis famil  
Q14007 schizosacch

107	7	2.0	493	1	RP54_ALCEU	P28615	alcaligenes	180	1.7	169	1	HLB2_ORYSA	O04985	oryza sativ
108	7	2.0	497	1	FXD2_HUMAN	O60548	homo sapien	181	1.7	172	1	NU6M_URIL0	P3208	uria lomvia
109	7	2.0	515	1	ROCA_BACSU	P39634	bacillus su	182	1.7	173	1	NU6M_AETCR	P3189	aethia cris
110	7	2.0	516	1	P34_ENTFC	P31692	enterococcu	183	1.7	173	1	NU6M_AETPU	P3190	aethia pui
111	7	2.0	523	1	P60_LISSE	Q01838	listeria se	184	1.7	173	1	NU6M_AETPY	P3191	aethia pygm
112	7	2.0	524	1	P60_LISIV	Q01837	listeria iv	185	1.7	173	1	NU6M_ALLAL	P3192	alle alle
113	7	2.0	527	1	HSF8_LYCPPE	P41153	lycopersico	186	1.7	173	1	NU6M_CALMA	P3196	callaris ma
114	7	2.0	551	1	CBX4_MOUSE	O55187	mus musculus	187	1.7	173	1	NU6M_CEPKO	P3197	cepphus gry
115	7	2.0	582	1	SPH2_HUMAN	Q92777	homo sapien	188	1.7	173	1	NU6M_CXCPG	P3198	cepphus col
116	7	2.0	617	1	SYN2_MOUSE	Q92777	homo sapien	189	1.7	173	1	NU6M_CXCPG	P3199	cyclophorhnc
117	7	2.0	633	1	PAN2_HUMAN	Q96rd6	homo sapien	190	1.7	173	1	NU6M_FRAAR	P3200	fraterculu
118	7	2.0	649	1	FAF1_RAT	Q924K2	rattus norv	191	1.7	173	1	NU6M_FRACR	P43201	fratercula
119	7	2.0	721	1	EZBE_HUMAN	Q13144	homo sapien	192	1.7	173	1	NU6M_LARCA	P41322	larus canus
120	7	2.0	766	1	AFK1_YEAST	P20134	saccharomyc	193	1.7	173	1	NU6M_LARCA	P41322	larus canus
121	7	2.0	799	1	SFLK_STRCO	P54741	streptomyce	194	1.7	173	1	NU6M_LUNCI	P43203	lunda cirrh
122	7	2.0	799	1	FXDA_HUMAN	P54741	streptomyce	195	1.7	173	1	NU6M_PTYAL	P43203	pythoromph
123	7	2.0	809	1	PAT3_CAEEL	Q27874	caenorhabdi	196	1.7	173	1	NU6M_STRCA	Q21407	struthio ca
124	7	2.0	815	1	MK07_HUMAN	Q13164	homo sapien	197	1.7	173	1	NU6M_SYNHV	P43206	synthlibora
125	7	2.0	830	1	GCL2_MOUSE	Q9jhd2	mus musculus	198	1.7	173	1	NU6M_SYNHV	P55734	escherichia
126	7	2.0	837	1	GCL2_MOUSE	Q92830	homo sapien	199	1.7	173	1	YCAP_ECOLI	P13589	r pituitary
127	7	2.0	882	1	GNDS_MOUSE	Q03385	mus musculus	200	1.7	173	1	PACA_RAT	O05261	mycobacteri
128	7	2.0	892	1	IF2_CHLTR	O84098	chlamydia t	201	1.7	173	1	VG49_BPML5	P02258	anser anser
129	7	2.0	914	1	GNDS_HUMAN	Q12967	homo sapien	202	1.7	173	1	H5_ANSA	P06513	cairina mos
130	7	2.0	950	1	DC12_DROME	Q12967	homo sapien	203	1.7	173	1	H5_CAIHO	P02254	saimo trutt
131	7	2.0	960	1	KIT_CHICK	P81870	drosophila	204	1.7	173	1	H1_SALTR	P08590	homo saplen
132	7	2.0	972	1	KFMS_HUMAN	Q08156	gallus gall	205	1.7	173	1	MLEV_HUMAN	Q05146	borderella
133	7	2.0	975	1	KFMS_HUMAN	P07333	homo sapien	206	1.7	173	1	OMPA_BORAV	O31701	bacillus su
134	7	2.0	975	1	KIT_CANFA	O97799	canis famil	207	1.7	173	1	MOBA_BACSU	P13249	streptomyce
135	7	2.0	975	1	KIT_MOUSE	P05532	mus musculus	208	1.7	173	1	PUAC_STRLP	O8260	versinia pe
136	7	2.0	976	1	KIT_MOUSE	P10721	homo sapien	209	1.7	173	1	YMBD_YEAST	P38429	saccharomyc
137	7	2.0	977	1	KFMS_MOUSE	P05581	mus musculus	210	1.7	173	1	CLP3_SYNY3	P74467	synecocyst
138	7	2.0	977	1	KIT_BOVIN	P43481	bos taurus	211	1.7	173	1	SOMA_PAGMA	P08591	pagrus majo
139	7	2.0	978	1	KFMS_RAT	Q00495	rattus norv	212	1.7	173	1	SOMA_PAGMA	O01282	acanthopagr
140	7	2.0	978	1	KIT_FELCI	Q28317	capra hircu	213	1.7	173	1	SOMA_PAGMA	O01283	lata calca
141	7	2.0	980	1	KFMS_FELCA	Q28317	capra hircu	214	1.7	173	1	SOMA_PAGMA	O01283	lata calca
142	7	2.0	1016	1	PMFH_CHLTR	P13369	felis silve	215	1.7	173	1	SOMA_PAGMA	O01283	lata calca
143	7	2.0	1083	1	T2D3_HUMAN	O48880	chlamydia t	216	1.7	173	1	SOMA_PAGMA	O01283	lata calca
144	7	2.0	1095	1	PIPA_DROME	O00268	homo sapien	217	1.7	173	1	SOMA_PAGMA	O01283	lata calca
145	7	2.0	1123	1	DC11_DROME	P13217	drosophila	218	1.7	173	1	SOMA_PAGMA	O01283	lata calca
146	7	2.0	1125	1	MDL_BORBU	O51568	borrelia bu	219	1.7	173	1	SOMA_PAGMA	O01283	lata calca
147	7	2.0	1131	1	YAB9_YEAST	P31380	saccharomyc	220	1.7	173	1	SOMA_PAGMA	O01283	lata calca
148	7	2.0	1147	1	YAB9_YEAST	P19706	acanthamoeb	221	1.7	173	1	SOMA_PAGMA	O01283	lata calca
149	7	2.0	1239	1	V120_EBV	P03189	epstein-bar	222	1.7	173	1	SOMA_PAGMA	O01283	lata calca
150	7	2.0	1274	1	MYPC_HUMAN	O14896	homo sapien	223	1.7	173	1	SOMA_PAGMA	O01283	lata calca
151	7	2.0	1298	1	VGR3_HUMAN	P35916	homo sapien	224	1.7	173	1	SOMA_PAGMA	O01283	lata calca
152	7	2.0	1323	1	LT23_CAEEL	P24348	caenorhabdi	225	1.7	173	1	SOMA_PAGMA	O01283	lata calca
153	7	2.0	1487	1	ICP4_HSVB	P28925	equine herp	226	1.7	173	1	SOMA_PAGMA	O01283	lata calca
154	7	2.0	1487	1	ICP4_HSVK	P17473	equine herp	227	1.7	173	1	SOMA_PAGMA	O01283	lata calca
155	7	2.0	1589	1	DC13_DROME	P18171	drosophila	228	1.7	173	1	SOMA_PAGMA	O01283	lata calca
156	7	2.0	1618	1	NEST_HUMAN	P48681	homo sapien	229	1.7	173	1	SOMA_PAGMA	O01283	lata calca
157	7	2.0	2156	1	RRPL_PUUMH	P27176	pumala vir	230	1.7	173	1	SOMA_PAGMA	O01283	lata calca
158	7	2.0	2220	1	CABI_HUMAN	Q9Y6J0	homo sapien	231	1.7	173	1	SOMA_PAGMA	O01283	lata calca
159	6	1.7	38	1	H5_COLLI	P02260	columba liv	232	1.7	173	1	SOMA_PAGMA	O01283	lata calca
160	6	1.7	72	1	SAS1_SPOHA	Q00213	sporosarcin	233	1.7	173	1	SOMA_PAGMA	O01283	lata calca
161	6	1.7	78	1	ACP_MYAXA	P80921	myxococcus	234	1.7	173	1	SOMA_PAGMA	O01283	lata calca
162	6	1.7	81	1	NU6M_ANAPL	Q06059	anas platyr	235	1.7	173	1	SOMA_PAGMA	O01283	lata calca
163	6	1.7	88	1	CU70_LOCOMI	P80232	locusta mig	236	1.7	173	1	SOMA_PAGMA	O01283	lata calca
164	6	1.7	92	1	VP10_NPVOP	P08357	orgyia pseu	237	1.7	173	1	SOMA_PAGMA	O01283	lata calca
165	6	1.7	113	1	RS6_SYNY3	P73636	synecocyst	238	1.7	173	1	SOMA_PAGMA	O01283	lata calca
166	6	1.7	115	1	VY1_TYLCU	P36282	tomato yell	239	1.7	173	1	SOMA_PAGMA	O01283	lata calca
167	6	1.7	118	1	RL7_MYCLU	P02395	micrococcu	240	1.7	173	1	SOMA_PAGMA	O01283	lata calca
168	6	1.7	121	1	KDGL_ECOLI	P00556	escherichia	241	1.7	173	1	SOMA_PAGMA	O01283	lata calca
169	6	1.7	122	1	IN17_HUMAN	P80516	araneus dia	242	1.7	173	1	SOMA_PAGMA	O01283	lata calca
170	6	1.7	126	1	CUT2_ARADI	P80516	araneus dia	243	1.7	173	1	SOMA_PAGMA	O01283	lata calca
171	6	1.7	129	1	RL7_CHLMU	P80001	chlamydia m	244	1.7	173	1	SOMA_PAGMA	O01283	lata calca
172	6	1.7	129	1	RL7_CHLTR	Q84310	chlamydia t	245	1.7	173	1	SOMA_PAGMA	O01283	lata calca
173	6	1.7	139	1	YL99_MYCTU	O40406	mycobacteri	246	1.7	173	1	SOMA_PAGMA	O01283	lata calca
174	6	1.7	142	1	YL22_ARCFU	O28158	archaeoglob	247	1.7	173	1	SOMA_PAGMA	O01283	lata calca
175	6	1.7	143	1	RS12_HORVU	Q9xhs0	hordeum vul	248	1.7	173	1	SOMA_PAGMA	O01283	lata calca
176	6	1.7	153	1	YC15_CAUCR	Q9a8v2	caulobacter	249	1.7	173	1	SOMA_PAGMA	O01283	lata calca
177	6	1.7	154	1	YGG9_YEAST	P53162	saccharomyc	250	1.7	173	1	SOMA_PAGMA	O01283	lata calca
178	6	1.7	157	1	CU19_LOCOMI	P45593	locusta mig	251	1.7	173	1	SOMA_PAGMA	O01283	lata calca
179	6	1.7	159	1	CU57_ARADI	P80519	araneus dia	252	1.7	173	1	SOMA_PAGMA	O01283	lata calca

O06836 streptomyce

253	1	1.7	250	1	1.7	326	6	1.7	353	1	PSBA_CUSRE	P32036 cuscuta ref
254	1	1.7	254	1	1.7	327	6	1.7	353	1	PSBA_MAGPY	O98735 magnolia py
255	1	1.7	255	1	1.7	328	6	1.7	353	1	PSBA_MEDSA	P04998 medicago sa
256	1	1.7	256	1	1.7	329	6	1.7	353	1	PSBA_ORYSA	P12094 oryza sativ
257	1	1.7	257	1	1.7	330	6	1.7	353	1	PSBA_ORYAC	P04848 nicotiana t
258	1	1.7	258	1	1.7	331	6	1.7	353	1	PSBA_ORYAC	P13910 vicia faba
259	1	1.7	259	1	1.7	332	6	1.7	353	1	PSBA_VICFA	Q3282 vigna ungu
260	1	1.7	260	1	1.7	333	6	1.7	354	1	PSBA_VIGUN	P51105 hordeum vul
261	1	1.7	261	1	1.7	334	6	1.7	354	1	PSBA_VIGUN	P05053 trypanosoma
262	1	1.7	262	1	1.7	335	6	1.7	354	1	PSBA_VIGUN	Q26736 trypanosoma
263	1	1.7	263	1	1.7	336	6	1.7	355	1	PSBA_VIGUN	P45370 c poly-beta
264	1	1.7	264	1	1.7	337	6	1.7	355	1	PSBA_VIGUN	P45366 t poly-beta
265	1	1.7	265	1	1.7	338	6	1.7	355	1	PSBA_VIGUN	P30692 neisseria s
266	1	1.7	266	1	1.7	339	6	1.7	355	1	PSBA_VIGUN	P55278 bacillus su
267	1	1.7	267	1	1.7	340	6	1.7	355	1	PSBA_VIGUN	Q95478 pseudomonas
268	1	1.7	268	1	1.7	341	6	1.7	355	1	PSBA_VIGUN	P57127 buchnera ap
269	1	1.7	269	1	1.7	342	6	1.7	355	1	PSBA_VIGUN	Q29715 archaeoglob
270	1	1.7	270	1	1.7	343	6	1.7	355	1	PSBA_VIGUN	Q24648 drosophila
271	1	1.7	271	1	1.7	344	6	1.7	355	1	PSBA_VIGUN	P34735 pichia angu
272	1	1.7	272	1	1.7	345	6	1.7	355	1	PSBA_VIGUN	P49669 trypanosoma
273	1	1.7	273	1	1.7	346	6	1.7	355	1	PSBA_VIGUN	P42712 streptomyce
274	1	1.7	274	1	1.7	347	6	1.7	355	1	PSBA_VIGUN	P11372 oryctolagus
275	1	1.7	275	1	1.7	348	6	1.7	355	1	PSBA_VIGUN	Q12708 sclerotinia
276	1	1.7	276	1	1.7	349	6	1.7	355	1	PSBA_VIGUN	Q48019 mycobacteri
277	1	1.7	277	1	1.7	350	6	1.7	355	1	PSBA_VIGUN	P06138 escherichia
278	1	1.7	278	1	1.7	351	6	1.7	355	1	PSBA_VIGUN	P57308 buchnera ap
279	1	1.7	279	1	1.7	352	6	1.7	355	1	PSBA_VIGUN	O51929 buchnera ap
280	1	1.7	280	1	1.7	353	6	1.7	355	1	PSBA_VIGUN	Q94144 sodalis glo
281	1	1.7	281	1	1.7	354	6	1.7	355	1	PSBA_VIGUN	P74724 synechocyst
282	1	1.7	282	1	1.7	355	6	1.7	355	1	PSBA_VIGUN	P58953 drosophila
283	1	1.7	283	1	1.7	356	6	1.7	355	1	PSBA_VIGUN	P24025 hepatitis b
284	1	1.7	284	1	1.7	357	6	1.7	355	1	PSBA_VIGUN	P12911 hepatitis b
285	1	1.7	285	1	1.7	358	6	1.7	355	1	PSBA_VIGUN	P03138 hepatitis b
286	1	1.7	286	1	1.7	359	6	1.7	355	1	PSBA_VIGUN	Q97139 hepatitis b
287	1	1.7	287	1	1.7	360	6	1.7	355	1	PSBA_VIGUN	Q97139 hepatitis b
288	1	1.7	288	1	1.7	361	6	1.7	355	1	PSBA_VIGUN	P43136 mus musculus
289	1	1.7	289	1	1.7	362	6	1.7	355	1	PSBA_VIGUN	O9017 rattus norv
290	1	1.7	290	1	1.7	363	6	1.7	355	1	PSBA_VIGUN	P45498 staphylococ
291	1	1.7	291	1	1.7	364	6	1.7	355	1	PSBA_VIGUN	O03340 mus musculus
292	1	1.7	292	1	1.7	365	6	1.7	355	1	PSBA_VIGUN	O03340 mus musculus
293	1	1.7	293	1	1.7	366	6	1.7	355	1	PSBA_VIGUN	Q43593 olea europae
294	1	1.7	294	1	1.7	367	6	1.7	355	1	PSBA_VIGUN	Q43593 olea europae
295	1	1.7	295	1	1.7	368	6	1.7	355	1	PSBA_VIGUN	Q43593 olea europae
296	1	1.7	296	1	1.7	369	6	1.7	355	1	PSBA_VIGUN	Q43593 olea europae
297	1	1.7	297	1	1.7	370	6	1.7	355	1	PSBA_VIGUN	Q43593 olea europae
298	1	1.7	298	1	1.7	371	6	1.7	355	1	PSBA_VIGUN	Q43593 olea europae
299	1	1.7	299	1	1.7	372	6	1.7	355	1	PSBA_VIGUN	Q43593 olea europae
300	1	1.7	300	1	1.7	373	6	1.7	355	1	PSBA_VIGUN	Q43593 olea europae
301	1	1.7	301	1	1.7	374	6	1.7	355	1	PSBA_VIGUN	Q43593 olea europae
302	1	1.7	302	1	1.7	375	6	1.7	355	1	PSBA_VIGUN	Q43593 olea europae
303	1	1.7	303	1	1.7	376	6	1.7	355	1	PSBA_VIGUN	Q43593 olea europae
304	1	1.7	304	1	1.7	377	6	1.7	355	1	PSBA_VIGUN	Q43593 olea europae
305	1	1.7	305	1	1.7	378	6	1.7	355	1	PSBA_VIGUN	Q43593 olea europae
306	1	1.7	306	1	1.7	379	6	1.7	355	1	PSBA_VIGUN	Q43593 olea europae
307	1	1.7	307	1	1.7	380	6	1.7	355	1	PSBA_VIGUN	Q43593 olea europae
308	1	1.7	308	1	1.7	381	6	1.7	355	1	PSBA_VIGUN	Q43593 olea europae
309	1	1.7	309	1	1.7	382	6	1.7	355	1	PSBA_VIGUN	Q43593 olea europae
310	1	1.7	310	1	1.7	383	6	1.7	355	1	PSBA_VIGUN	Q43593 olea europae
311	1	1.7	311	1	1.7	384	6	1.7	355	1	PSBA_VIGUN	Q43593 olea europae
312	1	1.7	312	1	1.7	385	6	1.7	355	1	PSBA_VIGUN	Q43593 olea europae
313	1	1.7	313	1	1.7	386	6	1.7	355	1	PSBA_VIGUN	Q43593 olea europae
314	1	1.7	314	1	1.7	387	6	1.7	355	1	PSBA_VIGUN	Q43593 olea europae
315	1	1.7	315	1	1.7	388	6	1.7	355	1	PSBA_VIGUN	Q43593 olea europae
316	1	1.7	316	1	1.7	389	6	1.7	355	1	PSBA_VIGUN	Q43593 olea europae
317	1	1.7	317	1	1.7	390	6	1.7	355	1	PSBA_VIGUN	Q43593 olea europae
318	1	1.7	318	1	1.7	391	6	1.7	355	1	PSBA_VIGUN	Q43593 olea europae
319	1	1.7	319	1	1.7	392	6	1.7	355	1	PSBA_VIGUN	Q43593 olea europae
320	1	1.7	320	1	1.7	393	6	1.7	355	1	PSBA_VIGUN	Q43593 olea europae
321	1	1.7	321	1	1.7	394	6	1.7	355	1	PSBA_VIGUN	Q43593 olea europae
322	1	1.7	322	1	1.7	395	6	1.7	355	1	PSBA_VIGUN	Q43593 olea europae
323	1	1.7	323	1	1.7	396	6	1.7	355	1	PSBA_VIGUN	Q43593 olea europae
324	1	1.7	324	1	1.7	397	6	1.7	355	1	PSBA_VIGUN	Q43593 olea europae
325	1	1.7	325	1	1.7	398	6	1.7	355	1	PSBA_VIGUN	Q43593 olea europae



399	1	1.7	414	1	COT2_HUMAN	P24468	homo sapien	472	1.7	502	1	CATA_PIG	O62839	sus scrofa
400	1	1.7	414	1	COT2_MOUSE	P43135	mus musculus	473	1.7	505	1	TCMO_CICAR	P01928	cicer ariet
401	1	1.7	414	1	COT2_RAT	O09018	rattus norv	474	1.7	506	1	CATA_BOVIN	P00432	bos taurus
402	1	1.7	414	1	CPTR_SOLTU	P29463	solanum tub	475	1.7	506	1	CATA_DRONE	P17336	drosophila
403	1	1.7	416	1	GLVA_HELPJ	O92mp7	helicobacte	476	1.7	507	1	IRX3_MOUSE	P81067	mus musculus
404	1	1.7	416	1	GLVA_HELPV	P56089	helicobacte	477	1.7	507	1	MEFA_HUMAN	O02078	homo sapien
405	1	1.7	419	1	G6AC_DROME	P83295	drosophila	478	1.7	510	1	YOT3_CAEL	P34649	caenorhabdi
406	1	1.7	420	1	O63A_DROME	O9vzw8	drosophila	479	1.7	511	1	COPD_BOVIN	P33619	bos taurus
407	1	1.7	420	1	PGKE_TRYBB	P08893	trypanosoma	480	1.7	511	1	COPD_HUMAN	P48444	homo sapien
408	1	1.7	420	1	PROA_NEIMA	O91uk8	neisseria m	481	1.7	513	1	WRK3_ARATH	O92q70	arabidopsis
409	1	1.7	420	1	PROA_NEIMB	O91zg3	neisseria m	482	1.7	513	1	GLCM_MOUSE	P17439	mus musculus
410	1	1.7	421	1	CC8_RAT	O8jhw5	rattus norv	483	1.7	516	1	EX7L_CHLTR	O84333	chlamydia t
411	1	1.7	421	1	PGKE_TRYBB	P07377	trypanosoma	484	1.7	520	1	LYN23_MYCTU	O10508	mycobacteri
412	1	1.7	421	1	VG2_BPIKE	P03660	bacterioph	485	1.7	522	1	LYN23_HAEIN	P44626	haemophilus
413	1	1.7	422	1	COT1_MOUSE	O60632	mus musculus	486	1.7	524	1	VG20_BPT4	P13334	bacterioph
414	1	1.7	422	1	PSDB_HUMAN	O00231	homo sapien	487	1.7	526	1	CATA_BRARE	O92q92	brachydanio
415	1	1.7	423	1	COT1_HUMAN	P10589	homo sapien	488	1.7	526	1	CATA_CANFA	O97492	canis famli
416	1	1.7	423	1	COT1_BOVIN	O98tr8	bos taurus	489	1.7	526	1	CATA_MOUSE	P04040	homo sapien
417	1	1.7	424	1	LMP2_CHICK	Q90617	gallus gall	490	1.7	526	1	CATA_MOUSE	P24270	mus musculus
418	1	1.7	425	1	YF26_MYCTU	Q50581	mycobacteri	491	1.7	527	1	CATA_RAT	P04762	rattus norv
419	1	1.7	426	1	FAB2_MOUSE	Q64733	mus musculus	492	1.7	527	1	CATA_RANRU	O9pwf7	rana rugosa
420	1	1.7	428	1	NXP1_HUMAN	O15818	homo sapien	493	1.7	527	1	HSF8_LYCES	Q40152	lycopersico
421	1	1.7	433	1	FTSZ_ARATH	Q42545	arabidopsis	494	1.7	528	1	MASY_EMENI	P28344	emerlicella
422	1	1.7	433	1	FTSZ_ECOLI	P06988	escherichia	495	1.7	528	1	V58K_BSMV	P04867	barley stri
423	1	1.7	434	1	HISX_PASNU	P95525	pasteurella	496	1.7	529	1	DHAL_ENTHI	Q30840	entamoeba h
424	1	1.7	434	1	HML_PASNU	P45546	escherichia	497	1.7	530	1	MATP_HUMAN	Q9umx9	homo sapien
425	1	1.7	434	1	YHFT_ECOLI	P35021	sulfolobus	498	1.7	533	1	MASY_ECOLI	P08997	escherichia
426	1	1.7	435	1	EFIA_SULSO	P26642	xenopus lae	499	1.7	534	1	P4HI_MOUSE	O60715	mus musculus
427	1	1.7	436	1	EFIG_XENLA	Q60175	methanococ	500	1.7	536	1	GLCM_HUMAN	P04062	homo sapien
428	1	1.7	436	1	SECY_METJA	O14209	homo sapien	501	1.7	540	1	TOP1_AQUAE	O66893	aquifex aeo
429	1	1.7	437	1	E2F2_HUMAN	P28541	methanococ	502	1.7	541	1	MASY_STRAL	O92h77	streptomyce
430	1	1.7	438	1	SECY_METVA	P36205	thermotoga	503	1.7	542	1	ZYX_CHICK	Q04584	gallus gall
431	1	1.7	439	1	GLNA_THEMEA	P07378	trypanosoma	504	1.7	543	1	MASY_STRAE	P77947	streptomyce
432	1	1.7	440	1	PGKC_TRYBB	P94337	corynebacte	505	1.7	546	1	MCP3_ECOLI	P05704	escherichia
433	1	1.7	442	1	FTSZ_CORGL	P38043	synechococ	506	1.7	547	1	ODP2_PSEAE	O59638	pseudomonas
434	1	1.7	443	1	NRTA_SYNP7	O37969	sus scrofa	507	1.7	552	1	AAK2_HUMAN	P54646	homo sapien
435	1	1.7	446	1	NV5R_PIG	Q83457	porcine ade	508	1.7	553	1	AAK2_RAT	Q09137	rattus norv
436	1	1.7	448	1	FIBP_ADRP3	O86574	aquifex aeo	509	1.7	553	1	NIFA_RHOCA	P09434	rhodobacter
437	1	1.7	450	1	HSLU_AQUAE	Q9nax8	trypanosoma	510	1.7	553	1	ODO2_MYCTU	Q10381	mycobacteri
438	1	1.7	452	1	ERF1_TRYBB	P09230	yarrowia li	511	1.7	556	1	FTHS_CLOCY	Q07064	clostridium
439	1	1.7	452	1	AEP_YARLI	Q12658	pneumocysti	512	1.7	557	1	ACHI_SCHGR	P23414	schistosom
440	1	1.7	454	1	IMDH_PNECA	O26134	methanobact	513	1.7	561	1	MASY_BRANA	P13244	brassica na
441	1	1.7	456	1	SECY_METTH	P21637	pseudomonas	514	1.7	563	1	SYR_STRPN	O54869	streptococ
442	1	1.7	459	1	COBG_PSEDE	P55055	homo sapien	515	1.7	564	1	ZYX_MOUSE	O62523	mus musculus
443	1	1.7	461	1	NRH2_HUMAN	P18825	homo sapien	516	1.7	566	1	GUNB_PAEIA	P23550	paenibacill
444	1	1.7	462	1	A2AC_HUMAN	O59342	enterobacte	517	1.7	566	1	MASY_CUCMA	P24571	cucurbita m
445	1	1.7	462	1	ENGA_ENTAE	O33212	mycobacteri	518	1.7	566	1	MASY_RAPSA	Q43827	raphanus sa
446	1	1.7	463	1	GSA_CHLRE	P19969	chlamydomon	519	1.7	567	1	MASY_GOSHI	P17432	gossypium h
447	1	1.7	464	1	AA5_RAT	P22165	rattus norv	520	1.7	568	1	CH60_BUGGR	O89216	cucumis gra
448	1	1.7	466	1	VL2_RHPV1	Q61398	rhesus papl	521	1.7	569	1	C972_SOYBN	Q39727	euglena gra
449	1	1.7	468	1	PCOI_MOUSE	O08628	rattus norv	522	1.7	576	1	CC18_SCHPO	O48921	glycine max
450	1	1.7	468	1	PCOI_RAT	P57074	gallus gall	523	1.7	577	1	POF3_SCHPO	P43411	schizosacch
451	1	1.7	470	1	SOXB_CHICK	O08628	rattus norv	524	1.7	577	1	FTSZ_AGRTU	O74991	schizosacch
452	1	1.7	472	1	YU87_MYCTU	P57074	gallus gall	525	1.7	583	1	RECN_SYNX3	O30992	agrobacteri
453	1	1.7	473	1	PSBC_MARPO	O53304	mycobacteri	526	1.7	584	1	DHSA_BACSU	P74374	synechocyst
454	1	1.7	477	1	SYC_RHIL0	P06414	marchantia	527	1.7	585	1	DAK2_YEAST	P08065	bacillus su
455	1	1.7	477	1	GS2_HUMAN	O984x8	rhizobium l	528	1.7	591	1	FTSZ_BACSU	P43550	saccharomyc
456	1	1.7	478	1	YVNC_HUMAN	Q9nmx5	homo sapien	529	1.7	592	1	FTSZ_BACSU	O31314	bartonella
457	1	1.7	478	1	YVNC_HUMAN	P04004	homo sapien	530	1.7	600	1	DNK3_BRYRH	Q05647	erysipeloth
458	1	1.7	478	1	YVNC_HUMAN	P33369	escherichia	531	1.7	601	1	DEAD_BUCAL	P57453	buchnera ap
459	1	1.7	483	1	YVNC_HUMAN	P42437	bacillus su	532	1.7	604	1	CIOI_MOUSE	P97414	mus musculus
460	1	1.7	484	1	YVNC_HUMAN	O91kq4	mus musculus	533	1.7	606	1	MM17_HUMAN	Q9u129	homo sapien
461	1	1.7	488	1	DGT1_HUMAN	O75907	homo sapien	534	1.7	608	1	UGST_ANTWA	O82627	antirrhinum
462	1	1.7	488	1	MM11_HUMAN	P24347	homo sapien	535	1.7	609	1	REAL_XENLA	Q01588	xenopus lae
463	1	1.7	490	1	MOT3_YEAST	P34785	saccharomyc	536	1.7	614	1	ODP2_HUMAN	P05151	h dihydrol
464	1	1.7	491	1	DGT1_CERAE	Q9gmfl	cercoptihet	537	1.7	614	1	YHQ3_ECOLI	P33553	escherichia
465	1	1.7	498	1	LYCB_CAPAN	Q43415	capsicum an	538	1.7	615	1	MUTA_MYCTU	P71773	mycobacteri
466	1	1.7	498	1	MEFA_MOUSE	Q60929	mus musculus	539	1.7	616	1	YGF_HUMAN	O15240	homo sapien
467	1	1.7	498	1	YAOI_SCHPO	Q10097	schizosacch	540	1.7	617	1	CYG2_HUMAN	O75343	homo sapien
468	1	1.7	500	1	LYCB_LYCES	Q43503	lycopersico	541	1.7	618	1	DNK3_STRCO	O05558	streptomyce
469	1	1.7	500	1	LYCB_TOBAC	Q43578	nicotiana t	542	1.7	618	1	DNK3_STRCO	Q54215	streptomyce
470	1	1.7	500	1	US24_HCMVA	P09700	human cytom	543	1.7	621	1	GIDA_BORBU	P33362	borrelia bu
471	1	1.7	501	1	XYLB_LACPE	P21939	lactobacill	544	1.7	626	1	HCY6_ANDAU	P80476	androctonus

545	1	1.7	626	1	PRIM_LISIN	Q92bq5 listeria in	618	1	HXA3_HAEIN	P45355 haemophilus
546	1	1.7	626	1	PRIM_LISMO	P47762 listeria mo	619	1	DNL1_HUMAN	P18858 homo sapien
547	6	1.7	630	6	ESAB_TRYEB	P23799 trypanosoma	620	1	HXA2_HAEIN	P45354 haemophilus
548	6	1.7	630	6	ESAB_TRYEQ	P26337 trypanosoma	621	1	CAIC_NOTVI	P91145 notophthalin
549	6	1.7	633	6	PBP2_ECOLI	P08150 escherichia	622	1	SLAP_CAMPE	P35827 campylobact
550	6	1.7	635	6	XYND_PABPO	P45796 paenibacilli	623	1	YK15_CAEEL	P46012 caenorhabdi
551	6	1.7	637	6	ODP2_AZOVI	P10802 azotobacter	624	1	XYNA_RUMPL	P29126 ruminococcu
552	6	1.7	641	6	PRIN_STRCO	Q9sin4 streptomyc	625	1	TSP4_HUMAN	P35443 homo sapien
553	6	1.7	644	6	C3AA_BACTT	P07130 bacillus th	626	1	SNXD_HUMAN	Q9y5w8 homo sapien
554	6	1.7	646	6	FLRI_HUMAN	Q9nzu1 homo sapien	627	1	SECA_CHLPN	Q9y765 chlamydia p
555	6	1.7	646	6	SR72_YEAST	P38688 saccharomyc	628	1	RHG6_HUMAN	O43182 homo sapien
556	6	1.7	647	6	YC46_HAEIN	P44135 haemophilus	629	1	PEX6_RAT	P54777 rattus norv
557	6	1.7	648	6	GCP4_DROME	Q9vku7 drosophila	630	1	GCP_CAEEL	Q10663 caenorhabdi
558	6	1.7	649	6	C3CA_BACTK	Q45744 bacillus th	631	1	PTPX_MACNE	Q02695 macaca neme
559	6	1.7	651	6	SE93_YEAST	P40357 saccharomyc	632	1	HMW1_MYCPN	Q50365 mycoplasma
560	6	1.7	652	6	C3BB_BACTU	Q06117 bacillus th	633	1	Y075_MYCPN	P75556 mycoplasma
561	6	1.7	652	6	NOS2_PARDE	Q51705 paracoccus	634	1	CPXB_BACME	P14779 bacillus me
562	6	1.7	656	6	YK79_MYCTU	Q10687 mycobacteri	635	1	P100_HCMVA	P08318 human cytom
563	6	1.7	670	6	SL52_RAT	P33792 rattus norv	636	1	CARB_PYRFU	Q8u085 pyrococcus
564	6	1.7	672	6	SL52_HUMAN	P31639 homo sapien	637	1	2PH1_DROME	P28166 drosophila
565	6	1.7	675	6	RG59_MOUSE	Q54828 mus musculu	638	1	DP0D_SOYBN	O48901 glycine max
566	6	1.7	677	6	RG59_MOUSE	P49805 rattus norv	639	1	S24C_SOYBN	P33992 homo sapien
567	6	1.7	682	6	CYG2_RAT	P22717 rattus norv	640	1	TFIG_HUMAN	Q92797 homo sapien
568	6	1.7	684	6	TC10_YEAST	P50273 saccharomyc	641	1	SPK_HUMAN	Q92797 homo sapien
569	6	1.7	692	6	AKA8_HUMAN	O43823 homo sapien	642	1	SRE1_HUMAN	P36956 homo sapien
570	6	1.7	692	6	HEXA_ANOGA	O17020 anopheles g	643	1	C8BA_BACUK	O45705 bacillus th
571	6	1.7	693	6	RECG_PASMU	Q9cmb4 pasteurella	644	1	DPOL_HSVT1	Q9yus3 herpesvirus
572	6	1.7	693	6	YETI_SCHPO	O14286 schizosacch	645	1	DPOL_HSVT2	Q9yus3 herpesvirus
573	6	1.7	695	6	PARE_CAUCR	O54479 caulobacter	646	1	NKX1_RAT	Q9qzm6 rattus norv
574	6	1.7	699	6	YGA_BACSU	P20166 bacillus su	647	1	PC12_HUMAN	Q9npq4 homo sapien
575	6	1.7	701	6	Y363_BUCAI	P57444 buchnera ap	648	1	RTN4_HUMAN	Q9npq3 homo sapien
576	6	1.7	704	6	NEUL_PIG	Q02038 sus scrofa	649	1	K125_CAEEL	O10925 caenorhabdi
577	6	1.7	704	6	T2D4_DROME	P45846 drosophila	650	1	CTD2_HUMAN	Q9ugb3 homo sapien
578	6	1.7	705	6	MLLC_STRCO	O88022 streptomyc	651	1	N121_HUMAN	Q9y2h3 homo sapien
579	6	1.7	706	6	DREB_MOUSE	Q9qxs6 mus musculu	652	1	NME3_HUMAN	Q92937 homo sapien
580	6	1.7	713	6	ZF2_MOUSE	P20239 mus musculu	653	1	NME3_MOUSE	Q00961 rattus norv
581	6	1.7	713	6	ERF2_CANAL	O13354 candida alb	654	1	NARG_ECOLI	Q01098 mus musculu
582	6	1.7	716	6	PBPB_BACSU	Q07868 bacillus su	655	1	CTD2_MOUSE	P09152 escherichia
583	6	1.7	717	6	PRDD_HUMAN	Q9h4q3 homo sapien	656	1	BXF_CLOBO	Q35927 mus musculu
584	6	1.7	722	6	Y290_HAEIN	P77868 haemophilus	657	6	GLP1_CAEEL	P30996 clostridium
585	6	1.7	730	6	G13A_DICDI	P34115 dictyosteli	658	1	XKDO_BACSU	P13508 caenorhabdi
586	6	1.7	735	6	DHR2_YEAST	P36009 saccharomyc	659	1	YME5_YEAST	Q44334 bacillus su
587	6	1.7	735	6	K6A1_RAT	Q63531 rattus norv	660	1	CTA1_RAT	P04693 saccharomyc
588	6	1.7	741	6	H0X1_HALRO	P28468 halocynthia	661	1	CTA1_HUMAN	P97846 rattus norv
589	6	1.7	742	6	TBX3_HUMAN	O15119 homo sapien	662	1	L112_CAEEL	P78357 homo sapien
590	6	1.7	750	6	PKNG_MYCTU	P96256 mycobacteri	663	1	VG65_HSVI1	Q9bv12 homo sapien
591	6	1.7	758	6	CHEA_RHME	Q52880 rhizobium m	664	1	IE18_PVKV1	P14585 caenorhabdi
592	6	1.7	760	6	METE_BUCAI	P57142 buchnera ap	665	1	IE18_PVKV1	Q00106 ictalurid h
593	6	1.7	763	6	METE_MYCLE	O05564 mycobacteri	666	1	IE18_PVKV1	P33479 pseudorabie
594	6	1.7	763	6	PKNG_MYCLE	P37993 mycobacteri	667	1	DPO3_STRPN	P11675 pseudorabie
595	6	1.7	788	6	HIR1_YEAST	P32479 saccharomyc	668	1	NME1_HUMAN	Q978q2 streptococc
596	6	1.7	795	6	TLR6_MOUSE	P25644 saccharomyc	669	1	NME1_MOUSE	Q12879 homo sapien
597	6	1.7	797	6	PAT1_YEAST	Q45755 bacillus th	670	1	NME1_MOUSE	P35436 mus musculu
598	6	1.7	803	6	CDAA_BACTU	Q45755 bacillus th	671	1	DPO3_STRPY	Q00959 rattus norv
599	6	1.7	803	6	SWI6_YEAST	P09959 saccharomyc	672	1	GSRI_HUMAN	Q9dfi9 streptococc
600	6	1.7	804	6	SYFB_BACSU	P17922 bacillus su	673	1	ABL_DROME	Q9nzm4 homo sapien
601	6	1.7	808	6	PDAL_PIMBR	O44883 pimipinella	674	1	YFJA_ECOLI	P00522 drosophila
602	6	1.7	808	6	PDAL_RICCO	Q41142 ricinus com	675	1	MY52_YEAST	P52143 escherichia
603	6	1.7	809	6	PDAL_TOBAC	P34000 nicotiana t	676	1	YU30_RALSO	P19524 saccharomyc
604	6	1.7	809	6	PDAL_VIGUN	O04855 vigna ungu	677	6	41_DROME	O8xv02 raistonias
605	6	1.7	822	6	EPS8_HUMAN	Q12929 homo sapien	678	1	PM20_CHLPN	Q9v8r9 drosophila
606	6	1.7	823	6	NSPI_YEAST	Q9udy8 homo sapien	679	1	MSPI_PLAYO	Q92812 chlamydia p
607	6	1.7	824	6	MLTI_HUMAN	P53532 corynebacte	680	1	YFA7_YEAST	P13828 plasmodium
608	6	1.7	824	6	CLPB_CORGL	Q9hcx4 homo sapien	681	1	SUIS_SUNMU	P43583 saccharomyc
609	6	1.7	824	6	TRP7_HUMAN	Q9wvc5 mus musculu	682	1	SHK3_RAT	O62653 suncus murl
610	6	1.7	862	6	TRP7_MOUSE	Q02910 drosophila	683	6	9A14_RAT	Q91404 rattus norv
611	6	1.7	862	6	CPN_DROME	Q02910 drosophila	684	1	FAS2_SCHPO	Q10289 s fatty aci
612	6	1.7	865	6	YJJA_YEAST	P40309 saccharomyc	685	1	BIG1_BOVIN	O46382 bos taurus
613	6	1.7	873	6	YJJA_YEAST	P53953 saccharomyc	686	1	BIG1_HUMAN	Q9y6d6 homo sapien
614	6	1.7	876	6	YFMS_YEAST	P34459 caenorhabdi	687	1	FAS2_CANAL	P43098 c fatty aci
615	6	1.7	880	6	YFMS_YEAST	Q12906 h interleuk	688	1	CYAA_YEAST	P08678 saccharomyc
616	6	1.7	894	6	ILF3_HUMAN	Q03866 rattus norv	689	1	Y233_HUMAN	Q92508 homo sapien
617	6	1.7	895	6	GNDS_RAT	O75891 homo sapien	690	1	RRPL_SYNV	P31332 sonchus yel

691	1.7	2144	1	GLT1_YEAST	Q12680	saccharomyc	764	1.5	73	1	H14_RABIT	P02252	oryctolagus
692	1.7	2298	1	CU05_HUMAN	Q93355	homo sapien	765	1.5	74	1	RPO2_HELPY	P25467	helicobacte
693	1.7	2332	1	POLG_FMDVA	P03308	f genome po	766	1.5	75	1	COXH_HUMAN	P09669	homo sapien
694	1.7	2332	1	POLG_FMDVA	P03308	f genome po	767	1.5	75	1	HMSA_SALSA	P09636	salmo salar
695	1.7	2333	1	POLG_FMDV1	P03306	f genome po	768	1.5	75	1	HOLI_BPRIT	Q38134	bacterioph
696	1.7	2504	1	FAS_HUMAN	P49327	homo sapien	769	1.5	75	1	RS21_BRUME	Q8Y445	brucella me
697	1.7	2505	1	FAS_RAT	P12785	rattus norv	770	1.5	75	1	Y261_BACHD	Q9K652	baecillus ha
698	1.7	2766	1	THYG_MOUSE	O08710	mus musculus	771	1.5	76	1	TXP6_APTSC	P4970	apostichus
699	1.7	2768	1	THYG_HUMAN	P01266	homo sapien	772	1.5	76	1	UBIQ_COPCO	P19848	coprinus co
700	1.7	3053	1	CAIC_HUMAN	P06882	rattus norv	773	1.5	76	1	UBIQ_SOYBN	P03993	glycine max
701	1.7	3058	1	CAIC_HUMAN	Q99715	homo sapien	774	1.5	76	1	UL79_HSV62	P52548	human herpe
702	1.7	3058	1	POLG_PEMVC	Q01500	p genome po	775	1.5	76	1	YB02_ARCFU	O29163	archaeoglob
703	1.7	3119	1	CAIC_MOUSE	Q60847	mus musculus	776	1.5	77	1	GEPB_BACSU	O06720	baecillus su
704	1.7	3206	1	POLG_PSBMV	P29152	p genome po	777	1.5	77	1	RL28_ECOLI	P02428	escherichia
705	1.7	3567	1	ERY2_SACER	Q03132	saccharopol	778	1.5	77	1	RL28_SALTY	O54325	salmonella
706	1.7	3674	1	SPCR_HUMAN	Q9NRC6	homo sapien	779	1.5	77	1	YGRG_BACFI	Q45132	baecillus fi
707	1.7	4273	1	PKSM_BACSU	P40972	baecillus su	780	1.5	78	1	CINA_STRGV	P29827	streptococc
708	1.7	4499	1	DYHA_CHLRE	Q39610	chlamydomon	781	1.5	78	1	RL28_PSEAE	Q9H2N8	pseudomonas
709	1.7	5217	1	HTSI_COCCA	Q01886	cochliobolu	782	1.5	79	1	CSMA_CHLAU	P09928	chloroflexu
710	1.5	14	1	UHA1_CANFA	P81162	clostridium	783	1.5	79	1	NSGX_HUMAN	Q9UH64	homo sapien
711	1.5	14	1	UN46_CLOPA	P81362	clostridium	784	1.5	79	1	POC1_BRARA	O42470	brassica ra
712	1.5	15	1	LEC2_PSOSC	P22585	psophocarpu	785	1.5	79	1	PSBH_CHLVU	P56323	chlorella v
713	1.5	15	1	PLAS_MICAE	P10625	microcystis	786	1.5	79	1	YKEF_ECOLI	P75677	escherichia
714	1.5	20	1	CD4_SHEEP	P05542	ovis aries	787	1.5	80	1	PYSL_ANASP	P07124	anabaena sp
715	1.5	22	1	ANFC_CHICK	P21805	gallus gall	788	1.5	82	1	CEP_VIBCH	Q9K323	vibrio chol
716	1.5	23	1	AU42_LITRA	P82398	litoria ran	789	1.5	82	1	CX7_NAJAT	P49122	naja atra (
717	1.5	27	1	ANF_ANGJA	P18144	anguilla ja	790	1.5	82	1	Y120_NPVOP	O10359	orgyia pseu
718	1.5	27	1	IPPD_MOUSE	Q60829	mus musculus	791	1.5	82	1	CX7A_NAJAT	O91126	naja atra (
719	1.5	28	1	PA2C_PSEPO	P20260	pseudechis	792	1.5	83	1	CX7P_NAJAT	O91996	naja atra (
720	1.5	30	1	UP61_UPEIN	P82037	uperoleia i	793	1.5	83	1	CXH_NAJNA	Q98P7	arabidopsis
721	1.5	30	1	UP62_UPEIN	P82038	uperoleia i	794	1.5	83	1	POC1_ARATH	Q91F54	arabidopsis
722	1.5	35	1	VORB_METTM	P80908	methanobact	795	1.5	83	1	POC2_ARATH	Q39406	brassica ra
723	1.5	36	1	ANFV_ANGJA	P22642	anguilla ja	796	1.5	84	1	EX7S_HAEIN	Q39414	haemophilus
724	1.5	36	1	RL6_HALCU	P05968	halobacteri	797	1.5	84	1	OAG1_SALTY	Q03032	salmonella
725	1.5	37	1	PSAJ_EUGGR	P30394	euglena gra	798	1.5	84	1	YPB3_ECOLI	P03851	escherichia
726	1.5	40	1	RPO_LSV	P27328	lily sympto	799	1.5	85	1	POC4_ALNGL	Q81701	alnus glutu
727	1.5	44	1	COAT_BPPE3	P03623	bacterioph	800	1.5	85	1	POC4_BEVE	Q39419	betula verr
728	1.5	44	1	PSAJ_PROMA	Q9X715	prochloroc	801	1.5	85	1	PYS1_FREDI	P11377	fremyella d
729	1.5	45	1	HEVP_HEVER	P80359	hevea bras	802	1.5	85	1	YCFR_ECOLI	P03780	bacterioph
730	1.5	46	1	CSPA_KLEPN	Q48493	klebsiella	803	1.5	85	1	YML5_PARTE	P75953	escherichia
731	1.5	47	1	RL32_HELPJ	Q92MM2	helicobacte	804	1.5	85	1	YML5_PARTE	P15616	paramecium
732	1.5	47	1	RL32_HELPY	P56054	helicobacte	805	1.5	85	1	RS21_CAUCR	Q9A387	caulobacter
733	1.5	50	1	PRVM_SCVCA	P35491	scyllorhinu	806	1.5	87	1	YBED_ECOLI	P30977	escherichia
734	1.5	51	1	MLEV_MOUSE	P09542	mus musculus	807	1.5	87	1	APC1_CANFA	P56595	canis fami
735	1.5	52	1	IPR_SOLME	P01078	solanum mel	808	1.5	88	1	APC1_MOUSE	P34928	mus muscu
736	1.5	52	1	RUBR_TREPA	Q83956	treponema p	809	1.5	88	1	APC1_MOUSE	P19939	rattus norv
737	1.5	52	1	YABO_ECOLI	P39221	escherichia	810	1.5	88	1	APC1_MOUSE	P19939	rattus norv
738	1.5	55	1	PHNS_DESVH	Q06173	desulfovibr	811	1.5	88	1	GP42_BRSP1	O48398	bacterioph
739	1.5	56	1	H2AQ_HUMAN	Q16777	homo sapien	812	1.5	88	1	H2A3_STRPU	P09530	strongyloce
740	1.5	57	1	HPI5_RHOGL	P38589	rhodopila g	813	1.5	88	1	RL37_CANAL	Q9P836	candida alb
741	1.5	60	1	HXB2_SALSA	P09638	salmo salar	814	1.5	88	1	RS21_RHILO	Q989Y4	rhizobium l
742	1.5	61	1	PPSA_ERWHE	O54457	erwinia her	815	1.5	88	1	VHED_BPIKE	P03670	bacterioph
743	1.5	62	1	CXH_NAJNA	P14541	naja naja k	816	1.5	88	1	Y874_CAUCR	P58091	caulobacter
744	1.5	62	1	SCX6_TITSE	P45669	tityus serr	817	1.5	89	1	YAYD_SCHPO	S10020	schizosacch
745	1.5	63	1	ANPL_AUSBR	P12100	austrorhizic	818	1.5	89	1	NTPL1_SPVKA	Q08513	swinepox vi
746	1.5	63	1	ANP2_AUSBR	P21001	austrorhizic	819	1.5	90	1	HXA2_NOTVI	P31261	notophthalm
747	1.5	63	1	YRKO_BACSU	P54431	baecillus su	820	1.5	90	1	Y169_RICPR	Q92QZ4	rickettsia
748	1.5	64	1	SAS4_BACSU	P04833	baecillus su	821	1.5	90	1	Y215_RICPR	Q92QV4	rickettsia
749	1.5	65	1	LHA3_RHOPA	P35103	rhodopsuendo	822	1.5	90	1	Y215_RICPR	P58095	escherichia
750	1.5	65	1	YP7A_TNVD	P27211	tobacco nec	823	1.5	91	1	VG76_BPM15	Q05291	mycobacteri
751	1.5	66	1	LHA2_RHOPA	P35102	rhodopsuendo	824	1.5	91	1	NODE_RHILV	P04685	rhizobium l
752	1.5	68	1	CYC3_DESAC	P00137	desulfuroumo	825	1.5	92	1	VGL1_HSV11	P06480	herpes simp
753	1.5	68	1	PLEX_PSEAM	Q9PRJ9	pseudopleur	826	1.5	92	1	Y886_METTH	O26972	methanobact
754	1.5	68	1	VHTJ_LAMBD	P03727	bacterioph	827	1.5	92	1	YSV3_CAEEL	Q10009	caenorhabdi
755	1.5	68	1	YLK5_CAEEL	P41953	caenorhabdi	828	1.5	93	1	REPI_ECOLI	P05830	escherichia
756	1.5	69	1	MOP_HAEIN	P45183	haemophilus	829	1.5	93	1	YQIC_CAEEL	Q09283	caenorhabdi
757	1.5	70	1	CSPI_ECOLI	P77605	escherichia	830	1.5	94	1	ASR1_YERPE	Q82665	yersinia pe
758	1.5	70	1	CSPI_SALTI	P58726	salmonella	831	1.5	94	1	ESA6_MYCTU	Q57165	mycobacteri
759	1.5	70	1	CSPO_SALTI	P39818	salmonella	832	1.5	95	1	YFI_ORYSA	O23810	oryza sativ
760	1.5	70	1	RS21_CAMJE	Q9PID2	campylobact	833	1.5	96	1	ABRB_BACSU	P08874	baecillus su
761	1.5	71	1	SASI_BACCE	P06551	baecillus ce	834	1.5	96	1	PRGB_HUMAN	Q02325	homo sapien
762	1.5	71	1	MBTH_MYCTU	O05821	mycobacteri	835	1.5	96	1	RL15_STRSC	P43415	streptomyce
763	1.5	71	1	V07K_PVXHB	Q07631	potato viru	836	1.5	97	1	FER2_CVACA	P15789	cyenidium c

837	1	1.5	97	1	KEFL_ECOLI	Q52281	escherichia
838	1	1.5	97	1	NUCC_SOYBN	P31174	glycine max
839	1	1.5	98	1	FIS_FASHA	O54367	pasteurella
840	1	1.5	98	1	MOBS_THIFE	P20086	thiobacillus
841	1	1.5	98	1	RS20_CHLMU	O9pjc4	chlamydia m
842	1	1.5	98	1	VHED_BPHHL	O07481	bacterioph
843	1	1.5	99	1	NIC1_HUMAN	O9ug19	homo sapien
844	1	1.5	99	1	PLAS_CUCPE	P00292	cucurbita p
845	1	1.5	99	1	RS20_CHLPN	O927f2	chlamydia p
846	1	1.5	99	1	ZJ33_MICE	P47475	mycoplasma
847	1	1.5	100	1	Y837_NEIMB	Q9jz25	neisseria m
848	1	1.5	100	1	YKPB_YEAST	P36055	saccharomyc
849	1	1.5	101	1	RS14_RHIME	Q92qf7	rhizobium m
850	1	1.5	101	1	YG75_MYCOP	P75117	mycoplasma
851	1	1.5	101	1	ARSC_NEIGO	P53534	neisseria g
852	1	1.5	102	1	FLAF_CAUCR	P21295	caulobacter
853	1	1.5	102	1	GLRX_RICCO	P55143	ricinus com
854	1	1.5	102	1	SECG_STRCO	Q9z521	streptomyce
855	1	1.5	102	1	TXOB_HADIN	Q9bjw0	hadronyche
856	1	1.5	102	1	Y224_METH	O26326	methanobact
857	1	1.5	103	1	ANFB_BOVIN	P13204	bos taurus
858	1	1.5	103	1	CHLB_NEPHX	P37850	nephrolepis
859	1	1.5	103	1	RL21_HAEIN	P43559	haemophilus
860	1	1.5	103	1	TCTA_HUMAN	P57738	homo sapien
861	1	1.5	103	1	YA46_NEIMA	Q9jv14	neisseria m
862	1	1.5	103	1	YEB4_ECOLI	P75301	mycoplasma
863	1	1.5	103	1	YGBQ_ECOLI	Q46894	escherichia
864	1	1.5	104	1	KAC6_RABIT	P03984	oryctolagus
865	1	1.5	104	1	LAC2_MOUSE	P01844	mus musculus
866	1	1.5	104	1	LAC2_RAT	P20767	rattus norv
867	1	1.5	104	1	LAC3_MOUSE	P01845	mus musculus
868	1	1.5	104	1	Y4EB_RHISN	P55425	rhizobium s
869	1	1.5	105	1	HXB4_BRARE	P22574	brachydanio
870	1	1.5	105	1	INS_SHEEP	P01318	ovis aries
871	1	1.5	105	1	LAC1_MOUSE	P01843	mus musculus
872	1	1.5	105	1	LAC_HUMAN	P01842	homo sapien
873	1	1.5	105	1	LAC_PIG	P01846	sus scrofa
874	1	1.5	105	1	LAC_RABIT	P01847	oryctolagus
875	1	1.5	105	1	YOPN_BACSU	Q34369	bacillus su
876	1	1.5	106	1	ATPR_DROME	O24407	drosophila
877	1	1.5	106	1	RL12_ARCFU	O28780	archaeoglob
878	1	1.5	106	1	THIO_SFPAU	P33791	streptomyce
879	1	1.5	106	1	VHSE_BPT3	P20322	bacterioph
880	1	1.5	106	1	YH80_YEAST	P38186	saccharomyc
881	1	1.5	107	1	CYC_APIME	P00341	apis mellif
882	1	1.5	107	1	GRO_HUMAN	O93e38	bruceella me
883	1	1.5	107	1	HIS2_BRUME	P06590	murine coro
884	1	1.5	107	1	T2AG_SCHPO	O74948	schizosacch
885	1	1.5	107	1	VNS2_CVMJH	Q9ckf3	pasteurella
886	1	1.5	107	1	YGB8_PASMU	P00030	eisenia foe
887	1	1.5	108	1	CYC_EISFO	P01315	sus scrofa
888	1	1.5	108	1	INS_PIG	Q46560	bacteroides
889	1	1.5	108	1	VAPI_BACNO	Q9zcc0	rickettsia
890	1	1.5	108	1	Y826_RICPR	O8xwk9	ralstonia s
891	1	1.5	108	1	Y065_RALSO	P00041	issatchenki
892	1	1.5	109	1	CYC_ISSOR	Q9mvv9	bos taurus
893	1	1.5	109	1	TRP5_BOVIN	P41420	autographa
894	1	1.5	109	1	Y005_NPVAC	P57825	pasteurella
895	1	1.5	109	1	Y205_PASMU	P17577	escherichia
896	1	1.5	109	1	YBAB_ECOLI	P58622	homo sapien
897	1	1.5	110	1	CUI5_HUMAN	P26541	human papil
898	1	1.5	110	1	VL3_HPVS5B	P33382	listeria mo
899	1	1.5	110	1	Y208_LISMO	P34328	caenorhabdi
900	1	1.5	110	1	YV21_YERPE	O8z896	yersinia pe
901	1	1.5	111	1	RL12_AERPE	Q9j3w9	aeropyrum p
902	1	1.5	111	1	RNPL_RANCA	P14626	rana catesb
903	1	1.5	111	1	Y546_SNY3	Q55397	synecocyst
904	1	1.5	111	1	YVDS_BACSU	O32262	bacillus su
905	1	1.5	111	1	COAD_BPFD	P03673	bacterioph
906	1	1.5	112	1	GLNB_RHET	O54053	rhizobium e
907	1	1.5	112	1	GLNB_RHOCA	P13556	rhodobacter
908	1	1.5	112	1	H2A3_LYTP1	P09589	lytechinus

910	1	1.5	112	1	KV2A_MOUSE	P01626	mus musculus
911	1	1.5	112	1	KV2D_MOUSE	P01629	mus musculus
912	1	1.5	112	1	PEDB_PEDAC	P36496	pediococcus
913	1	1.5	112	1	RBFA_MYCGE	P47389	mycoplasma
914	1	1.5	112	1	TGF2_BOVIN	P21214	bos taurus
915	1	1.5	112	1	YBAV_HAEIN	Q57134	haemophilus
916	1	1.5	113	1	FLIT_BACSU	P39740	bacillus su
917	1	1.5	113	1	KV2E_MOUSE	P03976	mus musculus
918	1	1.5	113	1	MEAL_PIG	Q95313	sus scrofa
919	1	1.5	113	1	RL12_HALVO	P41197	halobacteri
920	1	1.5	113	1	SSIF_STRBI	Q9r645	streptomyce
921	1	1.5	113	1	Y109_HAEIN	P43943	haemophilus
922	1	1.5	115	1	ACPM_MYCLE	O69475	mycobacteri
923	1	1.5	115	1	ACPM_MYCLE	Q10500	mycobacteri
924	1	1.5	115	1	SFP3_BOVIN	P04557	bos taurus
925	1	1.5	116	1	FLHD_PROMI	O34201	proteus mir
926	1	1.5	116	1	NU3M_MYTED	Q00568	mytilus edu
927	1	1.5	116	1	Y998_RHIME	P15550	strongyloce
928	1	1.5	116	1	ARSC_NEIMA	Q52966	rhizobium m
929	1	1.5	117	1	HV04_MOUSE	O9jqw0	neisseria m
930	1	1.5	117	1	WNT6_PLEJO	P01748	mus musculus
931	1	1.5	117	1	YFB9_YEAST	P28137	plethodon j
932	1	1.5	117	1	YFB9_YEAST	P43576	saccharomyc
933	1	1.5	118	1	GLBN_NOSCO	Q00812	nostoc comm
934	1	1.5	119	1	FLHD_YEREN	O86046	yersinia en
935	1	1.5	119	1	H2A4_PSAI	P07793	psammehinu
936	1	1.5	119	1	LAMR_PETMA	P33577	petromyzon
937	1	1.5	119	1	PA21_NAJOX	P25498	naja oxiana
938	1	1.5	119	1	RL17_BACSU	P20277	bacillus su
939	1	1.5	119	1	YD52_PASMU	O5cl88	pasturella
940	1	1.5	120	1	HPK_PSEPU	O87790	pseudomonas
941	1	1.5	120	1	INH_ERWCH	P18958	erwinia chr
942	1	1.5	120	1	KV2B_MOUSE	P01627	mus musculus
943	1	1.5	120	1	PHS_YEAST	P38744	saccharomyc
944	1	1.5	120	1	R18E_AERPE	Q9ybs1	aeropyrum p
945	1	1.5	120	1	RBFA_CAMJE	O9pi20	campylobact
946	1	1.5	120	1	RS20_DROME	P55838	drosophila
947	1	1.5	120	1	Y069_ARCFU	O30167	archaeoglob
948	1	1.5	120	1	YUTM_BACSU	O32113	bacillus su
949	1	1.5	121	1	ACPS_BACSU	P96618	bacillus su
950	1	1.5	121	1	ANFB_MOUSE	P40753	mus musculus
951	1	1.5	121	1	H2B_PATGR	P02284	patella gra
952	1	1.5	121	1	HK22_GUTH	O46899	guillardia
953	1	1.5	122	1	DBH_DEIRA	Q9r289	deinococcus
954	1	1.5	122	1	FMNB_DESYM	Q46604	desulfovibr
955	1	1.5	122	1	H2B1_PSAI	P02287	psammehinu
956	1	1.5	122	1	H2B_CAEEL	P04255	caenorhabdi
957	1	1.5	122	1	NRF1_SCHPO	Q9ur17	schizosacch
958	1	1.5	122	1	RL7_BACST	P05392	bacillus st
959	1	1.5	122	1	SMTE_SYNP7	P30340	synecococc
960	1	1.5	122	1	YF94_MYCPN	P75191	mycoplasma
961	1	1.5	123	1	H2A_DROME	P02267	drosophila
962	1	1.5	123	1	H2A_PARLI	P13630	paracentrot
963	1	1.5	123	1	H2A_PLADU	P19178	platynereis
964	1	1.5	123	1	H2A_SIPNU	P02270	sipunculus
965	1	1.5	123	1	H2A_STRPU	P02271	strongyloce
966	1	1.5	123	1	PA21_AKPI	P51972	agkistrodon
967	1	1.5	123	1	YNIA_KLEPN	P46382	klebsiella
968	1	1.5	124	1	FKBP_STRCH	P28725	streptomyce
969	1	1.5	124	1	H2A_ACRFO	P35061	acropora fo
970	1	1.5	124	1	H2A_ASTRU	P02269	asterias ru
971	1	1.5	124	1	H2A_SEPOF	P02268	septa offic
972	1	1.5	124	1	H2A_URECA	P27325	urechis cau
973	1	1.5	124	1	H2B_CHITH	P21897	chironomus
974	1	1.5	124	1	NOS_VICSA	Q41705	vicia sativ
975	1	1.5	124	1	YABJ_BACSU	P37552	bacillus su
976	1	1.5	124	1	YC69_MYCTU	Q11050	mycobacteri
977	1	1.5	125	1	H2A3_PSAI	P02265	psammehinu
978	1	1.5	125	1	H2AL_STRPU	P16886	strongyloce
979	1	1.5	125	1	LYC1_TACAC	P37156	tachyglossu
980	1	1.5	125	1	PCDS_HUMAN	O14737	homo sapien
981	1	1.5	125	1	PFDB_HALN1	Q9Hsh0	halobacteri
982	1	1.5	125	1	PLAS_SYNP7	P55020	synecococc



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RX MEDLINE-84108348; PubMed-6363059;
RA Braun G., Cole S.T.;
RT "Molecular characterization of the gene coding for major outer
RL membrane protein Ompa from Enterobacter aerogenes.";
RL Eur. J. Biochem. 137:495-500(1983).
CC -1- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE
CC STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A
CC RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A PORIN
CC WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
CC SOLUTES (BY SIMILARITY).
CC -1- SUBUNIT: MONOMER (PROBABLE).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -1- SIMILARITY: BELONGS TO THE OMPA FAMILY.
CC -----
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CC -----
DR EMBL: X00254; CAA25062.1;
DR PIR: S07222; S07222.
DR HSP; P02934; IQJP.
DR InterPro: IPR001145; Bac_OmpA.
DR Pfam: PF00691; OmpA; 1.
DR PRINTS: PR01021; OmpA_membrane; 1.
DR PRODOM: PD000930; Bac_OmpA; 1.
DR PROSITE: PS01068; OmpA; 1.
DR Outer membrane; Transmembrane; Phage recognition; Signal; Repeat;
KW Porin.
FT SIGNAL 1 21
FT CHAIN 22 350 OUTER MEMBRANE PROTEIN A.
FT TRANSMEM 27 40 POTENTIAL.
FT TRANSMEM 59 71 POTENTIAL.
FT TRANSMEM 74 89 POTENTIAL.
FT TRANSMEM 101 111 POTENTIAL.
FT TRANSMEM 115 130 POTENTIAL.
FT TRANSMEM 145 157 POTENTIAL.
FT TRANSMEM 163 179 POTENTIAL.
FT TRANSMEM 185 196 POTENTIAL.
FT DOMAIN 205 212 4 X 2 AA TANDEM REPEATS OF A-P.
FT REPEAT 205 206 1.
FT REPEAT 207 208 2.
FT REPEAT 209 210 3.
FT REPEAT 211 212 4.
FT DOMAIN 261 305 OMPA-LIKE.
FT DISULFID 315 327 BY SIMILARITY.
SQ SEQUENCE 350 AA; 37575 MW; 6276C6F2F21065DA CRC64;

Query Match 15.4%; Score 53; DB 1; Length 350;
Best Local Similarity 100.0%; Pred. No. 2.7e-47;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 213 FTLKSDVLFNFNFKATLKPEQQALDQLYTQLSNWDKGSAAVVLGYTDRIGSE 265
Db 219 FTLKSDVLFNFNFKATLKPEQQALDQLYTQLSNWDKGSAAVVLGYTDRIGSE 271

RESULT 3
OMPA_CITFR
ID OMPA_CITFR STANDARD; PRT; 238 AA.
AC P24016;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Outer membrane protein A (Outer membrane protein II) (Fragment).
GN OMPA.
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

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OC Citrobacter.
OX NCBI_TaxID=546;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-OS60;
RX MEDLINE-92065252; PubMed-1955870;
RA Lawrence J.G., Ochman H., Hartl D.L.;
RT "Molecular and evolutionary relationships among enteric bacteria.";
RL J. Gen. Microbiol. 137:1911-1921(1991).
CC -1- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE
CC STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A
CC RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A PORIN
CC WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
CC SOLUTES (BY SIMILARITY).
CC -1- SUBUNIT: MONOMER (PROBABLE).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -1- SIMILARITY: BELONGS TO THE OMPA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M63354; AAA23095.1;
DR HSP; P02934; IQJP.
DR InterPro: IPR001145; Bac_OmpA.
DR Pfam: PF00691; OmpA; 1.
DR PRINTS: PR01021; OmpA_membrane; 1.
DR PRODOM: PD000930; Bac_OmpA; 1.
DR PROSITE: PS01068; OmpA; 1.
DR Outer membrane; Transmembrane; Phage recognition; Repeat; Porin.
KW Porin.
FT SIGNAL 1 1
FT CHAIN 2 8 POTENTIAL.
FT TRANSMEM 12 27 POTENTIAL.
FT TRANSMEM 43 54 POTENTIAL.
FT TRANSMEM 60 76 POTENTIAL.
FT TRANSMEM 82 93 POTENTIAL.
FT DOMAIN 104 109 3 X 2 AA TANDEM REPEATS OF A-P.
FT REPEAT 104 105 1.
FT REPEAT 106 107 2.
FT REPEAT 108 109 3.
FT DOMAIN 158 202 OMPA-LIKE.
FT DISULFID 212 224 BY SIMILARITY.
FT NON_TER 238 238
SQ SEQUENCE 238 AA; 25664 MW; 66EAL36D73A3F286 CRC64;

Query Match 12.5%; Score 43; DB 1; Length 238;
Best Local Similarity 100.0%; Pred. No. 5.2e-37;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 KISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKG 334
Db 195 KISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKG 237

RESULT 4
OMPA_ECOLI
ID OMPA_ECOLI STANDARD; PRT; 346 AA.
AC P02934;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Outer membrane protein A precursor (Outer membrane protein II*).
GN OMPA OR TOLG OR TUT OR CON OR B0957 OR 21307 OR Ecs1041.
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562, 83334;

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RA [1] SEQUENCE FROM N.A.  
RA STRAIN-K12;  
RX MEDLINE-81053729; PubMed-6253901;  
RA Beck E., Bremer E.;  
RT "Nucleotide sequence of the gene ompA coding the outer membrane  
RL protein II of Escherichia coli K-12";  
RL Nucleic Acids Res. 8:3011-3024(1980).  
RN [2]  
RA SEQUENCE FROM N.A.  
RA STRAIN-K12;  
RX MEDLINE-81170587; PubMed-6260961;  
RA Morva N.R., Nakamura K., Inouye M.;  
RT "Gene structure of the OmpA protein, a major surface protein of  
RL Escherichia coli required for cell-cell interaction";  
RL J. Mol. Biol. 143:317-328(1980).  
RN [3]  
RA SEQUENCE FROM N.A.  
RA STRAIN-K12;  
RX MEDLINE-97426617; PubMed-9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shaoy Y.;  
RT "The complete genome sequence of Escherichia coli K-12";  
RL Science 277:1232-1244(1997).  
RN [4]  
RA SEQUENCE FROM N.A.  
RA STRAIN-K12;  
RX MEDLINE-97061202; PubMed-8905232;  
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,  
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,  
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,  
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,  
RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,  
RA Yano M., Horiuchi T.;  
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome  
RL corresponding to the 12.7-28.0 min region on the linkage map";  
RL DNA Res. 3:137-155(1996).  
RN [5]  
RA SEQUENCE FROM N.A.  
RA STRAIN-O157:H7 / EDL933 / ATCC 700927;  
RX MEDLINE-21074935; PubMed-11206551;  
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,  
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
RA Posfai G., Hackett J., Klink S., Boutin A., Shaoy Y., Miller L.,  
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamocousis K.,  
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
RA Welch R.A., Blattner F.R.;  
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";  
RL Nature 409:529-533(2001).  
RN [6]  
RA SEQUENCE FROM N.A.  
RA STRAIN-O157:H7 / RIMD 0509952;  
RX MEDLINE-21156231; PubMed-11258796;  
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,  
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,  
RA Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,  
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;  
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli  
RL O157:H7 and genomic comparison with a laboratory strain K-12";  
RL DNA Res. 8:11-22(2001).  
RN [7]  
RA SEQUENCE OF 22-346.  
RA STRAIN-K12;  
RX MEDLINE-81054820; PubMed-7001461;  
RA Chen R., Schmidmayr W., Kramer C., Chen-Schweissner U., Henning U.;  
RT "Primary structure of major outer membrane protein II (ompA protein)  
RL of Escherichia coli K-12";  
RL Proc. Natl. Acad. Sci. U.S.A. 77:4592-4596(1980).  
RN [8]  
RA SEQUENCE OF 22-32.  
RA STRAIN-K12 / W3110;  
RA Pasquali C., Sanchez J.-C., Ravier F., Golaz O., Hughes G.J.,  
RA Frutiger S., Paquet N., Wilkins M., Appel R.D., Baloch A.,  
RA Hochstrasser D.F.;  
RL Submitted (SEP-1994) to the SWISS-PROT data bank.  
RN [9]  
RA SEQUENCE OF 22-34.  
RA STRAIN-K12 / EMG2;  
RX MEDLINE-97443975; PubMed-9298646;  
RA Link A.J., Robison K., Church G.M.;  
RT "Comparing the predicted and observed properties of proteins encoded  
RL in the genome of Escherichia coli K-12";  
RL Electrophoresis 18:1259-1313(1997).  
RN [10]  
RA SEQUENCE OF 22-26.  
RA STRAIN-K12 / W3110;  
RX MEDLINE-98291876; PubMed-9629924;  
RA Molloy M.P., Herbert B.R., Walsh B.J., Tyler M.I., Traini M.,  
RA Sanchez J.-C., Hochstrasser D.F., Williams K.L., Gooley A.A.;  
RT "Extraction of membrane proteins by differential solubilization for  
RL separation using two-dimensional gel electrophoresis";  
RL Electrophoresis 19:837-844(1998).  
RN [11]  
RA MUTANTS RESISTANT TO PHAGE ENTRY.  
RX MEDLINE-84264337; PubMed-6086577;  
RA Morona R., Klose M., Henning U.;  
RT "Escherichia coli K-12 outer membrane protein (OmpA) as a  
RL bacteriophage receptor: analysis of mutant genes expressing altered  
RL proteins";  
RL J. Bacteriol. 159:570-578(1984).  
RN [12]  
RA MUTANTS RESISTANT TO PHAGE ENTRY.  
RX MEDLINE-86033606; PubMed-3902787;  
RA Morona R., Kramer C., Henning U.;  
RT "Bacteriophage receptor area of outer membrane protein OmpA of  
RL Escherichia coli K-12";  
RL J. Bacteriol. 164:539-543(1985).  
RN [13]  
RA PORIN ACTIVITY.  
RX STRAIN-K12;  
RX MEDLINE-92129334; PubMed-1370823;  
RA Sugawara E., Nikaido H.;  
RT "Pore-forming activity of OmpA protein of Escherichia coli";  
RL J. Biol. Chem. 267:2507-2511(1992).  
RN [14]  
RA TOPOLOGY.  
RX MEDLINE-94148615; PubMed-8106193;  
RA Gromiha M.M., Ponnuswamy P.K.;  
RT "Prediction of transmembrane beta-strands from hydrophobic  
RL characteristics of proteins";  
RL Int. J. Pept. Protein Res. 42:420-431(1993).  
RN [15]  
RA TOPOLOGY.  
RX MEDLINE-99296577; PubMed-10368142;  
RA Koebnik R.;  
RT "Structural and functional roles of the surface-exposed loops of the  
RL beta-barrel membrane protein OmpA from Escherichia coli";  
RL J. Bacteriol. 181:3688-3694(1999).  
RN [16]  
RA X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 22-192.  
RX MEDLINE-99023200; PubMed-9808047;  
RA Pautsch A., Schulz G.E.;  
RT "Structure of the outer membrane protein A transmembrane domain";  
RL Nat. Struct. Biol. 5:1013-1017(1998).  
RN [17]  
RA X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS).  
RX MEDLINE-20229895; PubMed-10764596;  
RA Pautsch A., Schulz G.E.;  
RT "High-resolution structure of the OmpA membrane domain";  
RL J. Mol. Biol. 298:273-282(2000).  
RN [18]  
RA MASS SPECTROMETRY.  
RX MEDLINE-2022957; PubMed-10757971;  
RA le Coutre J., Whitelegge J.P., Gross A., Turk E., Wright E.M.,

RA Kaback H.R., Faull K.F.,  
RT "Proteomics on full-length membrane proteins using mass  
RL spectrometry";  
CC -1- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE  
CC STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A  
CC RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A PORIN  
CC WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL  
CC SOLUTES.  
CC -1- SUBUNIT: MONOMER (PROBABLE).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.  
CC -1- MASS SPECTROMETRY: MW=35177; METHOD=Electrospray; RANGE=22-346.  
CC -1- SIMILARITY: BELONGS TO THE OMPA FAMILY.  
CC  
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CC  
CC EMBL: V00307; CAA23588.1; -;  
CC EMBL: AE000198; AAC74043.1; -;  
CC EMBL: D90733; BAA35715.1; -;  
CC EMBL: D90734; BAA35722.1; -;  
CC EMBL: AE005286; AAG55443.1; -;  
CC EMBL: AP002554; BAB34464.1; -;  
CC PIR: A03434; MMECA.  
CC PDB: 1BXW; 30-DEC-98.  
CC PDB: 1QJP; 30-JUN-00.  
CC SWISS-2DPAGE; P02934; COLI.  
CC ECO2DBASE; F024.5; 6TH EDITION.  
CC ECO2DBASE; F028.0; 6TH EDITION.  
CC ECO2DBASE; F033.0; 6TH EDITION.  
CC ECO2DBASE; F033.1; 6TH EDITION.  
CC EcoGene; EGI0669; ompA.  
CC InterPro: IPR001145; Bac\_OmpA.  
CC InterPro: IPR000498; OmpA\_tmem.  
CC Pfam; PF00691; OmpA; 1.  
CC PRINTS; PR01021; OMPADOMAIN.  
CC

Query Match 9.6%; Score 33; DB 1; Length 346;  
Best Local Similarity 100.0%; Pred. No. 2e-26;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 87 KAQGVQLTAKLGYPIITDDLDIYRLGGMVVRAD 119  
DB 94 KAQGVQLTAKLGYPIITDDLDIYRLGGMVVRAD 126  
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RESULT 5  
OMPA\_ESCFE STANDARD; PRT; 243 AA.  
AC P24754;  
DT 01-MAR-1992 (Rel. 21, Created)  
DT 01-MAR-1992 (Rel. 21, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Outer membrane protein A (Outer membrane protein II) (Fragment).  
GN OMPA.  
OS Escherichia hermannii.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=565;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 33650, and ATCC 33652;  
RX MEDLINE=92065252; PubMed=1955870;  
RA Lawrence J.G., Ochman H., Hartl D.L.;  
RT "Molecular and evolutionary relationships among enteric bacteria";  
RL J. Gen. Microbiol. 137:1911-1921(1991).  
CC -1- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE

CC STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A  
CC RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A PORIN  
CC WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL  
CC SOLUTES (BY SIMILARITY).  
CC -1- SUBUNIT: MONOMER (PROBABLE).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.  
CC -1- SIMILARITY: BELONGS TO THE OMPA FAMILY.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL: M63346; AAA24234.1; -;  
CC EMBL: M63347; AAA24238.1; -;  
CC HSP; P02934; IBXW.  
CC InterPro: IPR001145; Bac\_OmpA.  
CC InterPro: IPR000498; OmpA\_tmem.  
CC Pfam; PF00691; OmpA; 1.  
CC Pfam; PF01389; OmpA\_membrane; 1.  
CC ProDom; PD000930; Bac\_OmpA; 1.  
CC ProSite; PS01068; OMPA; 1.  
KW Outer membrane; Transmembrane; Phage recognition; Repeat; Porin.  
FT NON\_TER 1  
FT TRANSMEM <1 8 POTENTIAL.  
FT TRANSMEM 12 27 POTENTIAL.  
FT TRANSMEM 47 58 POTENTIAL.  
FT TRANSMEM 64 80 POTENTIAL.  
FT TRANSMEM 86 97 POTENTIAL.  
FT DOMAIN 107 114 4 X 2 AA TANDEM REPEATS OF A-P.  
FT REPEAT 107 108 1.  
FT REPEAT 109 110 2.  
FT REPEAT 111 112 3.  
FT REPEAT 113 114 4.  
FT DOMAIN 163 207 OMPA-LIKE.  
FT DISULFID 217 229 BY SIMILARITY.  
FT NON\_TER 243 243  
SQ SEQUENCE 243 AA; 26202 MW; AA6CB6BA390D1E9D CRC64;  
Query Match 8.4%; Score 29; DB 1; Length 243;  
Best Local Similarity 100.0%; Pred. No. 2.1e-22;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 210 TKHFTLKSDVLFNFNFKATLKPEGQALDQ 238  
DB 118 TKHFTLKSDVLFNFNFKATLKPEGQALDQ 146  
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RESULT 6  
OMPA\_ESCFE STANDARD; PRT; 243 AA.  
AC P24747;  
DT 01-MAR-1992 (Rel. 21, Created)  
DT 01-MAR-1992 (Rel. 21, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Outer membrane protein A (Outer membrane protein II) (Fragment).  
GN OMPA.  
OS Escherichia fergusonii.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=564;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 35471, ATCC 35469, and ATCC 35472;  
RX MEDLINE=92065252; PubMed=1955870;  
RA Lawrence J.G., Ochman H., Hartl D.L.;  
RT "Molecular and evolutionary relationships among enteric bacteria";  
RL J. Gen. Microbiol. 137:1911-1921(1991).  
CC -1- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE  
CC STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A



```
CC RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A PORIN
CC WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
CC SOLUTES (BY SIMILARITY).
CC -|- SUBUNIT: MONOMER (PROBABLE).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC AND ATCC 35471.
CC -|- SIMILARITY: BELONGS TO THE OMPA FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: M63352; AAA24236.1; -
CC EMBL: M63351; AAA24232.1; -
CC EMBL: M63353; AAA24240.1; -
CC HSSP: P02934; IQJP.
CC InterPro: IPR001145; Bac_OmpA.
CC InterPro: IPR000498; OmpA_tmem.
CC Pfam: PF00691; OmpA; 1.
CC Pfam: PF01389; OmpA_membrane; 1.
CC ProDom: PD000930; Bac_OmpA; 1.
CC ProSite: PS01068; OmpA; 1.
CC Outer membrane; Transmembrane; Phage recognition; Repeat; Porin.
CC NON_TER 1 1
CC TRANSMEM <1 8 POTENTIAL.
CC TRANSMEM 12 27 POTENTIAL.
CC TRANSMEM 48 59 POTENTIAL.
CC TRANSMEM 65 81 POTENTIAL.
CC TRANSMEM 87 98 POTENTIAL.
CC DOMAIN 107 114 4 X 2 AA TANDEM REPEATS OF A-P.
CC REPEAT 107 108 1.
CC REPEAT 109 110 2.
CC REPEAT 111 112 3.
CC REPEAT 113 114 4.
CC DOMAIN 163 207 OMPA-LIKE.
CC DISULFID 217 229 BY SIMILARITY.
CC VARIANT 39 39 E -> D (IN STRAIN ATCC 35469).
CC NON_TER 243 243
CC SEQUENCE 243 AA; B89F7FC29D42E3AB CRC64;
CC
CC Query Match 7.8%; Score 27; DB 1; Length 243;
CC Best Local Similarity 100.0%; Pred. No. 2.6e-20;
CC Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 93 LTAKLGYPIITDDLDIYTRLGGMVWRAD 119
CC Db 1 LTAKLGYPIITDDLDIYTRLGGMVWRAD 27
CC
CC RESULT 7
CC OMPA_SHIDY STANDARD; PRT; 351 AA.
CC ID OMPA_SHIDY
CC AC P02935;
CC DT 21-JUL-1986 (Rel. 01, Created)
CC DT 21-JUL-1986 (Rel. 01, Last sequence update)
CC DT 01-NOV-1995 (Rel. 32, Last annotation update)
CC DE Outer membrane protein A precursor (Outer membrane protein II).
CC GN OMPA.
CC OS Shigella dysenteriae.
CC OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
CC OC Shigella.
CC OX NCB1_TaxID=622;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=82221414; PubMed=6283478;
CC RA Braun G., Cole S.T.;
CC RT "The nucleotide sequence coding for major outer membrane protein OmpA
CC of Shigella dysenteriae.";
```

```
RL Nucleic Acids Res. 10:2367-2378(1982).
CC -|- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE
CC STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A
CC RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A PORIN
CC WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
CC SOLUTES (BY SIMILARITY).
CC -|- SUBUNIT: MONOMER (PROBABLE).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -|- SIMILARITY: BELONGS TO THE OMPA FAMILY.
CC
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CC
CC EMBL: V01344; CAA24638.1; -
CC PIR: A03435; MNEBAD.
CC HSSP: P02934; IQJP.
CC InterPro: IPR001145; Bac_OmpA.
CC InterPro: IPR000498; OmpA_tmem.
CC Pfam: PF00691; OmpA; 1.
CC Pfam: PF01389; OmpA_membrane; 1.
CC PRINTS: PR01021; OMPADOMAIN.
CC ProDom: PD000930; Bac_OmpA; 1.
CC ProSite: PS01068; OmpA; 1.
CC Outer membrane; Transmembrane; Phage recognition; Signal; Repeat;
CC Porin.
CC SIGNAL 1 21
CC CHAIN 22 351 OUTER MEMBRANE PROTEIN A.
CC TRANSMEM 27 40 POTENTIAL.
CC TRANSMEM 55 67 POTENTIAL.
CC TRANSMEM 70 85 POTENTIAL.
CC TRANSMEM 97 107 POTENTIAL.
CC TRANSMEM 111 126 POTENTIAL.
CC TRANSMEM 147 158 POTENTIAL.
CC TRANSMEM 164 180 POTENTIAL.
CC TRANSMEM 186 197 POTENTIAL.
CC DOMAIN 206 213 4 X 2 AA TANDEM REPEATS OF A-P.
CC REPEAT 206 207 1.
CC REPEAT 208 209 2.
CC REPEAT 210 211 3.
CC REPEAT 212 213 4.
CC DOMAIN 262 306 OMPA-LIKE.
CC DISULFID 316 328 BY SIMILARITY.
CC SEQUENCE 351 AA; 37741 MW; 1499AA5F5395B35B CRC64;
CC
CC Query Match 7.0%; Score 24; DB 1; Length 351;
CC Best Local Similarity 100.0%; Pred. No. 4.8e-17;
CC Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 210 TKHFTLKSDVLFNFNKATLKPEGQ 233
CC Db 217 TKHFTLKSDVLFNFNKATLKPEGQ 240
CC
CC RESULT 8
CC OMPA_SALTY STANDARD; PRT; 350 AA.
CC ID OMPA_SALTY
CC AC P02936;
CC DT 21-JUL-1986 (Rel. 01, Created)
CC DT 15-JUN-2002 (Rel. 41, Last sequence update)
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC DE Outer membrane protein A precursor (Outer membrane protein 33k) (Outer
CC membrane major heat-modifiable protein).
CC GN OMPA OR STM1070.
CC OS Salmonella typhimurium.
CC OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
CC OC Salmonella.
CC OX NCB1_TaxID=602;
CC RN [1]
```

SEQUENCE FROM N.A.  
 RX MEDLINE=83287368; PubMed=6349993;  
 RA Freidl R., Cole S.T.;  
 RT "Cloning and molecular characterization of the ompA gene from  
 RL *Salmonella typhimurium*,"  
 RN Eur. J. Biochem. 134:497-502(1983).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;  
 RX MEDLINE=21534948; PubMed=11677609;  
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,  
 RA Waterston R., Wilson R.K.;  
 RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium  
 LT2,"  
 RN Nature 413:852-856(2001).  
 CC -1- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE  
 CC STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A  
 CC RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A PORIN  
 CC WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL  
 CC SOLUTES (BY SIMILARITY).  
 CC -1- SUBUNIT: MONOMER (PROBABLE).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.  
 CC -1- SIMILARITY: BELONGS TO THE OMPA FAMILY.  
 CC  
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 CC  
 CC EMBL: X02006; CAA26037.1; -  
 CC EMBL: AE08746; AAL20003.1; -  
 CC PIR: A03436; MMEBAT.  
 CC HSP: P02934; IQJP.  
 CC StyGene; SG10263; ompA.  
 CC InterPro: IPR001145; Bac\_OmpA.  
 CC InterPro: IPR000498; OmpA\_tmam.  
 CC Pfam: PF00691; OmpA; 1.  
 CC Pfam: PF01389; OmpA\_membrane; 1.  
 CC ProDom: PD000930; Bac\_OmpA; 1.  
 CC PROSITE: PS01068; OmpA; 1.  
 CC Outer membrane; Transmembrane; Phage recognition; Signal; Repeat;  
 KW Porin; Complete proteome.  
 FT SIGNAL 1 21  
 FT CHAIN 22 350 OUTER MEMBRANE PROTEIN A.  
 FT TRANSMEM 27 40 POTENTIAL.  
 FT TRANSMEM 55 67 POTENTIAL.  
 FT TRANSMEM 70 85 POTENTIAL.  
 FT TRANSMEM 97 107 POTENTIAL.  
 FT TRANSMEM 111 126 POTENTIAL.  
 FT TRANSMEM 146 157 POTENTIAL.  
 FT TRANSMEM 163 179 POTENTIAL.  
 FT TRANSMEM 185 196 POTENTIAL.  
 FT DOMAIN 205 212 4 X 2 AA TANDEM REPEATS OF A-P.  
 FT REPEAT 205 206 1.  
 FT REPEAT 207 208 2.  
 FT REPEAT 209 210 3.  
 FT REPEAT 211 212 4.  
 FT DOMAIN 261 305 OMPA-LIKE.  
 FT DISULFID 315 327 BY SIMILARITY.  
 FT CONFLICT 114 114 V -> F (IN REF. 1).  
 FT CONFLICT 247 247 S -> I (IN REF. 1).  
 SQ SEQUENCE 350 AA; 37515 MW; B4AC52C8C5DF54FE CRC64;  
 Query Match 6.4%; Score 22; DB 1; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-15;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 KISARGMGESNPVTGNTCDNVK 313  
 |||||||||||||||||||  
 Db 298 KISARGMGESNPVTGNTCDNVK 319  
 |||||||||||||||||||  
 RESULT 9  
 OMPA\_ESCBL STANDARD; PRT; 241 AA.  
 ID OMPA\_ESCBL  
 AC Q99124; Q03617;  
 DT 01-NOV-1987 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Outer membrane protein A (Outer membrane protein II) (Fragment).  
 GN OMPA.  
 OS *Escherichia blattae*.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC *Escherichia*.  
 OX NCBI\_TaxID=563;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 33429, ATCC 29907, and ATCC 33430;  
 RX MEDLINE=92065252; PubMed=1955870;  
 RA Lawrence J.G., Ochman H., Hartl D.L.;  
 RT "Molecular and evolutionary relationships among enteric bacteria,"  
 RL J. Gen. Microbiol. 137:1911-1921(1991).  
 CC -1- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE  
 CC STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A  
 CC RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A PORIN  
 CC WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL  
 CC SOLUTES (BY SIMILARITY).  
 CC -1- SUBUNIT: MONOMER (PROBABLE).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.  
 CC -1- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF STRAIN ATCC 33429.  
 CC -1- SIMILARITY: BELONGS TO THE OMPA FAMILY.  
 CC  
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 CC  
 CC EMBL: M63343; AAA24235.1; -  
 CC EMBL: M63344; AAA24239.1; -  
 CC EMBL: M63345; AAA24242.1; -  
 CC HSP: P02934; IQJP.  
 CC InterPro: IPR001145; Bac\_OmpA.  
 CC InterPro: IPR000498; OmpA\_tmam.  
 CC Pfam: PF00691; OmpA; 1.  
 CC Pfam: PF01389; OmpA\_membrane; 1.  
 CC ProDom: PD000930; Bac\_OmpA; 1.  
 CC PROSITE: PS01068; OmpA; 1.  
 CC Outer membrane; Transmembrane; Phage recognition; Repeat; Porin.  
 FT NON\_TER 1 1  
 FT TRANSMEM <1 8 POTENTIAL.  
 FT TRANSMEM 12 27 POTENTIAL.  
 FT TRANSMEM 46 57 POTENTIAL.  
 FT TRANSMEM 63 79 POTENTIAL.  
 FT TRANSMEM 85 96 POTENTIAL.  
 FT DOMAIN 105 112 4 X 2 AA TANDEM REPEATS OF A-P.  
 FT REPEAT 105 106 1.  
 FT REPEAT 107 108 2.  
 FT REPEAT 109 110 3.  
 FT REPEAT 111 112 4.  
 FT DOMAIN 161 205 OMPA-LIKE.  
 FT DISULFID 215 227 BY SIMILARITY.  
 FT VARIANT 33 33 V -> G (IN STRAIN ATCC 29907).  
 FT VARIANT 56 56 W -> M (IN STRAIN ATCC 33430).  
 FT VARIANT 101 101 MISSING (IN STRAIN ATCC 33430).  
 FT VARIANT 103 103 N -> S (IN STRAIN ATCC 29907 AND  
 FT STRAIN ATCC 33430).  
 FT VARIANT 220 220 K -> Q (IN STRAIN ATCC 29907 AND



```
FT REPEAT 106 107 2.
FT REPEAT 108 109 3.
FT REPEAT 110 111 4.
FT REPEAT 112 113 5.
FT DISULFID 215 229 BY SIMILARITY.
FT NON_TER 243 243
SQ SEQUENCE 243 AA; 25972 MW; 687CC9C10DDEC64C CRC64;

Query Match
Best Local Similarity 4.9%; Score 17; DB 1; Length 243;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 LKPEGQALDQLYTOLS 244
DB 135 LKPEGQALDQLYTOLS 151

RESULT 12
ID OMPA_BUCAI STANDARD; PRT; 349 AA.
AC P57414;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE OmpA-like protein precursor.
GN OMPA OR BU332
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum symbiotic bacterium).
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=118099;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tokyo 1998;
RX MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. APS.";
RL Nature 407:81-86(2000).
CC -1- FUNCTION: ACTS AS A PORIN WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL SOLUTES (BY SIMILARITY).
CC -1- SUBUNIT: MONOMER (PROBABLE).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE OMPA FAMILY.
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CC -----
DR EMBL; AF001119; BAB13037.1; -.
DR HSSP; P02934; IQJP.
DR InterPro; IPR001145; Bac_OmpA.
DR InterPro; IPR000498; OmpA_tmnm.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA_membrane; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR ProDom; PD000930; Bac_OmpA; 1.
DR PROSITE; PS01068; OMPA; FALSE_NEG.
KW Transmembrane; Porin; Signal; Complete proteome.
FT SIGNAL 1 22
FT CHAIN 23 349 POTENTIAL.
FT TRANSMEM 27 40 POTENTIAL.
FT TRANSMEM 63 75 POTENTIAL.
FT TRANSMEM 78 93 POTENTIAL.
FT TRANSMEM 106 116 POTENTIAL.
FT TRANSMEM 120 135 POTENTIAL.
FT TRANSMEM 154 165 POTENTIAL.
FT TRANSMEM 171 187 POTENTIAL.
FT TRANSMEM 193 204 POTENTIAL.
FT DOMAIN 207 218 HINGE LIKE.
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FT DOMAIN 267 311 OMPA-LIKE.
FT DISULFID 321 333 BY SIMILARITY.
SQ SEQUENCE 349 AA; 39303 MW; CC14AB1BD590CF58 CRC64;

Query Match
Best Local Similarity 3.5%; Score 12; DB 1; Length 349;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 321 CLAPDRRVEIEV 332
DB 333 CLAPDRRVEIEV 344

RESULT 13
ID OM52_HAEIN STANDARD; PRT; 353 AA.
AC P38368;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Outer membrane protein P5 precursor (OMP P5).
GN OMPA OR OMPp5.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 22-34.
RC STRAIN=1613 / Serotype B;
RX MEDLINE=93366472; PubMed=8359929;
RA Munson R.S. Jr., Grass S., West R.;
RT "Molecular cloning and sequence of the gene for outer membrane protein P5 of Haemophilus influenzae.";
RL Infect. Immun. 61:4017-4020(1993).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -1- SIMILARITY: BELONGS TO THE OMPA FAMILY.
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CC -----
DR EMBL; L20309; AAA03346.1; -.
DR HSSP; P02934; IQJP.
DR InterPro; IPR001145; Bac_OmpA.
DR InterPro; IPR000498; OmpA_tmnm.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA_membrane; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR ProDom; PD000930; Bac_OmpA; 1.
DR PROSITE; PS01068; OMPA; 1.
KW Outer membrane; Transmembrane; Porin; Signal.
FT SIGNAL 1 21
FT CHAIN 22 353 OUTER MEMBRANE PROTEIN P5.
FT DISULFID 326 338 BY SIMILARITY.
FT DOMAIN 272 316 OMPA-LIKE.
SQ SEQUENCE 353 AA; 37594 MW; E58A659E786D0D0F7 CRC64;

Query Match
Best Local Similarity 2.9%; Score 10; DB 1; Length 353;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 321 CLAPDRRVEI 330
DB 338 CLAPDRRVEI 347

RESULT 14
ID OM53_HAEIN STANDARD; PRT; 359 AA.
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AC P45996;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Outer membrane protein P5 precursor (OMP P5) (Fimbrin).
GN OMPA OR OMPPS.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus
OC NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=NTHI 1128;
RX MEDLINE=94222575; PubMed=7909539;
RA Sirakova T., Kollatukudy P.E., Murwin D., Billy J., Leake E.,
RT Lim D., Demaria T., Bakaletz L.;
"Role of fimbriae expressed by nontypeable Haemophilus influenzae in
pathogenesis of and protection against otitis media and relatedness
of the fimbria subunit to outer membrane protein A.";
RL Infect. Immun. 62:2002-2020(1994).
CC -1- FUNCTION: ACTS AS A FIMBRIAE SUBUNIT.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -1- SIMILARITY: BELONGS TO THE OMPA FAMILY.
CC -----
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CC -----
DR EMBL; L08448; AAA24959.1; -
DR HSP; P02934; IBXW.
DR InterPro: IPR001145; Bac_OmpA.
DR InterPro: IPR000498; OmpA_tmem.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA_membrane; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRODOM; PD000830; Bac_OmpA; 1.
DR PROSITE; PS01068; OMPA; FALSE_NEG.
KW Outer membrane; Transmembrane; Porin; Signal; Fimbria.
FT SIGNAL 1 21
FT CHAIN 22 359 OUTER MEMBRANE PROTEIN P5.
FT DISULFID 332 344 BY SIMILARITY.
FT DOMAIN 278 322 OMPA-LIKE.
SQ SEQUENCE 359 AA; 38340 MW; 576B1C59B4818C37 CRC64;

Query Match 2.9%; Score 10; DB 1; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 321 CLAPDRRVEI 330
DB 344 CLAPDRRVEI 353
|||||

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## RESULT 15

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MLE1_MUGCA
ID MLE1_MUGCA STANDARD; PRT; 186 AA.
AC P82159;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myosin light chain 1, skeletal muscle isoform (Al catalytic) (Alkali)
DE (LC-1) (LC1).
OS Mugil capito (Grey mullet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Mugilomorpha; Mugilidae;
OC Liza.
OX NCBI_TaxID=30804;
RN [1]

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RP SEQUENCE.
RC TISSUE=Fast muscle;
RX MEDLINE=92042685; PubMed=1939601;
RA Dalla Libera L., Carpenne E., Theibert J., Collins J.H.;
RT "Fish myosin alkali light chains originate from two different genes.";
RL J. Muscle Res. Cell Motil. 12:366-371(1991).
CC -1- SUBUNIT: MYOSIN IS A HEXAMER OF 2 HEAVY CHAINS & 4 LIGHT CHAINS.
CC -1- MISCELLANEOUS: IN FISH, MYOSIN MLC1 AND MLC3 APPEAR TO BE PRODUCED
CC BY TWO DIFFERENT GENES UNLIKE IN BIRDS AND MAMMALS, WHERE THEY ARE
CC PRODUCED FROM A SINGLE GENE BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, BUT THIS
CC PROTEIN DOES NOT BIND CALCIUM.
DR HSP; P02607; 1BR1.
DR InterPro: IPR002048; EF-hand.
DR Pfam; PF00036; efhand; 2.
DR PRODOM; PD000012; EF-hand; 2.
KW Myosin; Muscle protein.
FT MOD_RES 1 1
SQ SEQUENCE 186 AA; 20067 MW; 57306F13CDE9E639 CRC64;
BLOCKED.

Query Match 2.6%; Score 9; DB 1; Length 186;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 APAPAPAPE 207
DB 12 APAPAPAPE 20
|||||

```

Search completed: April 15, 2003, 08:55:36  
Job time : 41 secs

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: April 15, 2003, 08:51:59 ; Search time 34 Seconds  
(without alignments)  
2084.712 Million cell updates/sec

Title: US-09-831-061-2

Perfect score: 344

Sequence: 1 MKAIFVLNAPKDNWTYAGG.....DRRVEIEVKGKVEVTPAG 344

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 5

Total number of hits satisfying chosen parameters: 39383

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

SPTREMBL\_21.\*

1: sp\_archaea.\*

2: sp\_bacteria.\*

3: sp\_fungi.\*

4: sp\_human.\*

5: sp\_invertebrate.\*

6: sp\_mammal.\*

7: sp\_mhc.\*

8: sp\_organelle.\*

9: sp\_phage.\*

10: sp\_plant.\*

11: sp\_rhodent.\*

12: sp\_virus.\*

13: sp\_vertebrate.\*

14: sp\_unclassified.\*

15: sp\_rvirus.\*

16: sp\_bacteriap.\*

17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	15.4	238	Q91114	Q91114 escherichia
2	36	10.5	238	Q91123	Q91123 enterobacte
3	33	9.6	148	Q93Q71	Q93Q71 erwinia per
4	33	9.6	246	Q91618	Q91618 shigella fl
5	29	8.4	244	Q47880	Q47880 escherichia
6	29	8.4	244	Q91115	Q91115 escherichia
7	28	8.1	148	Q93QR2	Q93QR2 erwinia psi
8	28	8.1	148	Q93QR1	Q93QR1 erwinia psi
9	28	8.1	148	Q93QR0	Q93QR0 erwinia psi
10	28	8.1	148	Q93QR0	Q93QR0 erwinia psi
11	28	8.1	149	Q93QR4	Q93QR4 erwinia psi
12	28	8.1	149	Q93QR3	Q93QR3 erwinia psi
13	26	7.6	149	Q93QR2	Q93QR2 erwinia rha
14	22	6.4	147	Q93QR6	Q93QR6 brenneria r
15	22	6.4	149	Q93QR5	Q93QR5 erwinia mal
16	22	6.4	149	Q93QR4	Q93QR4 erwinia mal

17	22	6.4	346	2	Q916J0	Q916J0 escherichia
18	22	6.4	350	16	Q827S0	Q827S0 salmonella
19	22	6.4	353	16	Q82G77	Q82G77 versinia pe
20	21	6.1	147	2	Q93Q88	Q93Q88 erwinia chr
21	21	6.1	149	2	Q93Q85	Q93Q85 erwinia mal
22	21	6.1	149	2	Q93Q84	Q93Q84 erwinia tra
23	21	6.1	149	2	Q93Q80	Q93Q80 erwinia tra
24	20	5.8	249	2	Q93Q87	Q93Q87 brenneria r
25	20	5.8	249	2	Q91619	Q91619 salmonella
26	19	5.5	147	2	Q93Q83	Q93Q83 erwinia tra
27	19	5.5	147	2	Q93Q82	Q93Q82 erwinia tra
28	19	5.5	149	2	Q93Q83	Q93Q83 erwinia tra
29	19	5.5	149	2	Q93Q82	Q93Q82 erwinia tra
30	19	5.5	149	2	Q93Q82	Q93Q82 erwinia tra
31	19	5.5	149	2	Q93Q82	Q93Q82 erwinia tra
32	19	5.5	149	2	Q93Q82	Q93Q82 erwinia tra
33	19	5.5	149	2	Q93Q82	Q93Q82 erwinia tra
34	19	5.5	149	2	Q93Q82	Q93Q82 erwinia tra
35	19	5.5	149	2	Q93Q82	Q93Q82 erwinia tra
36	19	5.5	149	2	Q93Q82	Q93Q82 erwinia tra
37	19	5.5	149	2	Q93Q82	Q93Q82 erwinia tra
38	19	5.5	149	2	Q93Q82	Q93Q82 erwinia tra
39	19	5.5	149	2	Q93Q82	Q93Q82 erwinia tra
40	19	5.5	149	2	Q93Q82	Q93Q82 erwinia tra
41	19	5.5	149	2	Q93Q82	Q93Q82 erwinia tra
42	19	5.5	149	2	Q93Q82	Q93Q82 erwinia tra
43	19	5.5	149	2	Q93Q82	Q93Q82 erwinia tra
44	19	5.5	149	2	Q93Q82	Q93Q82 erwinia tra
45	19	5.5	149	2	Q93Q82	Q93Q82 erwinia tra
46	19	5.5	149	2	Q93Q82	Q93Q82 erwinia tra
47	19	5.5	149	2	Q93Q82	Q93Q82 erwinia tra
48	19	5.5	149	2	Q93Q82	Q93Q82 erwinia tra
49	19	5.5	149	2	Q93Q82	Q93Q82 erwinia tra
50	19	5.5	149	2	Q93Q82	Q93Q82 erwinia tra
51	19	5.5	149	2	Q93Q82	Q93Q82 erwinia tra
52	19	5.5	149	2	Q93Q82	Q93Q82 erwinia tra
53	19	5.5	149	2	Q93Q82	Q93Q82 erwinia tra
54	19	5.5	149	2	Q93Q82	Q93Q82 erwinia tra
55	19	5.5	149	2	Q93Q82	Q93Q82 erwinia tra
56	19	5.5	149	2	Q93Q82	Q93Q82 erwinia tra
57	19	5.5	149	2	Q93Q82	Q93Q82 erwinia tra
58	19	5.5	149	2	Q93Q82	Q93Q82 erwinia tra
59	19	5.5	149	2	Q93Q82	Q93Q82 erwinia tra
60	19	5.5	149	2	Q93Q82	Q93Q82 erwinia tra
61	18	5.2	146	2	Q93Q85	Q93Q85 erwinia tra
62	18	5.2	146	2	Q93Q85	Q93Q85 erwinia tra
63	18	5.2	146	2	Q93Q85	Q93Q85 erwinia tra
64	18	5.2	146	2	Q93Q85	Q93Q85 erwinia tra
65	18	5.2	146	2	Q93Q85	Q93Q85 erwinia tra
66	18	5.2	146	2	Q93Q85	Q93Q85 erwinia tra
67	18	5.2	146	2	Q93Q85	Q93Q85 erwinia tra
68	18	5.2	146	2	Q93Q85	Q93Q85 erwinia tra
69	17	4.9	149	2	Q93Q84	Q93Q84 erwinia tra
70	17	4.9	149	2	Q93Q84	Q93Q84 erwinia tra
71	16	4.7	147	2	Q93Q84	Q93Q84 erwinia tra
72	15	4.4	145	2	Q93Q84	Q93Q84 erwinia tra
73	15	4.4	145	2	Q93Q84	Q93Q84 erwinia tra
74	15	4.4	145	2	Q93Q84	Q93Q84 erwinia tra
75	15	4.4	145	2	Q93Q84	Q93Q84 erwinia tra
76	15	4.4	145	2	Q93Q84	Q93Q84 erwinia tra
77	15	4.4	145	2	Q93Q84	Q93Q84 erwinia tra
78	15	4.4	145	2	Q93Q84	Q93Q84 erwinia tra
79	14	4.1	145	2	Q93Q84	Q93Q84 erwinia tra
80	14	4.1	145	2	Q93Q84	Q93Q84 erwinia tra
81	14	4.1	145	2	Q93Q84	Q93Q84 erwinia tra
82	14	4.1	145	2	Q93Q84	Q93Q84 erwinia tra
83	14	4.1	145	2	Q93Q84	Q93Q84 erwinia tra
84	14	4.1	145	2	Q93Q84	Q93Q84 erwinia tra
85	14	4.1	145	2	Q93Q84	Q93Q84 erwinia tra
86	14	4.1	145	2	Q93Q84	Q93Q84 erwinia tra
87	14	4.1	145	2	Q93Q84	Q93Q84 erwinia tra
88	14	4.1	145	2	Q93Q84	Q93Q84 erwinia tra
89	14	4.1	145	2	Q93Q84	Q93Q84 erwinia tra

90	14	4.1	149	2	Q93056	Q93q56 erwinia amy	163	8	2.3	92	10	Q24350	Q24350 silene lati
91	14	4.1	149	2	Q93054	Q93q54 erwinia amy	164	8	2.3	94	16	Q8X6U0	Q8X6U0 escherichia
92	14	4.1	149	2	Q93053	Q93q53 erwinia amy	165	8	2.3	97	10	Q8S017	Q8S017 oryza sativ
93	14	4.1	149	2	Q93050	Q93q50 erwinia amy	166	8	2.3	129	2	Q57111	Q57111 veillonella
94	14	4.1	149	2	Q930R9	Q93qr9 erwinia amy	167	8	2.3	131	10	Q94A23	Q94a23 arabidopsis
95	14	4.1	149	2	Q930R5	Q93qr5 erwinia amy	168	8	2.3	131	10	Q92T19	Q92t19 arabidopsis
96	13	3.8	147	2	Q930N5	Q93qn5 brenneria s	169	8	2.3	134	2	Q54030	Q54030 propionigen
97	13	3.8	149	2	Q9A073	Q9aq73 erwinia amy	170	8	2.3	140	10	Q8RZM6	Q8Rz6 oryza sativ
98	12	3.5	150	2	Q930N9	Q93qn9 pectobacter	171	8	2.3	142	2	Q9L5A0	Q9L5A0 hellobacter
99	11	3.2	147	2	Q930N6	Q93qn6 brenneria s	172	8	2.3	145	5	Q45192	Q45192 caenorhabdi
100	11	3.2	147	2	Q930N4	Q93qn4 brenneria s	173	8	2.3	147	2	Q69087	Q69087 hellobacter
101	11	3.2	147	2	Q930N3	Q93qn3 brenneria s	174	8	2.3	163	16	Q9A6B3	Q9A6b3 caulobacter
102	11	3.2	147	2	Q930N2	Q93qn2 brenneria s	175	8	2.3	164	13	Q90W45	Q90w45 decapteris
103	11	3.2	147	2	Q930N1	Q93qn1 brenneria s	176	8	2.3	165	2	Q54279	Q54279 saccharopol
104	10	2.9	106	2	Q9R659	Q9r659 proteus mir	177	8	2.3	166	5	Q9NFX6	Q9nf6 ceratitidis c
105	10	2.9	236	5	Q9VDH1	Q9vdx1 drosophila	178	8	2.3	166	5	Q62008	Q62008 ceratitidis c
106	10	2.9	339	2	Q44298	Q44298 aeromonas s	179	8	2.3	170	5	Q9VX77	Q9vx77 drosophila
107	10	2.9	341	2	Q8RJ58	Q8rj58 haemophilus	180	8	2.3	172	13	Q9IB35	Q9ib35 katusonug
108	10	2.9	344	2	Q8RMW2	Q8rmw2 haemophilus	181	8	2.3	181	10	Q9ZRE9	Q9zre9 arabidopsis
109	10	2.9	344	2	Q8RMW1	Q8rmw1 haemophilus	182	8	2.3	182	16	Q9CBW9	Q9cbw9 mycobacteri
110	10	2.9	344	2	Q8RMW0	Q8rmw0 haemophilus	183	8	2.3	185	16	Q8XXW2	Q8xxw2 raiatonia s
111	10	2.9	344	2	Q8RML9	Q8rml9 haemophilus	184	8	2.3	190	5	P90955	P90955 caenorhabdi
112	10	2.9	344	2	Q8RML8	Q8rml8 haemophilus	185	8	2.3	192	13	Q90895	Q90895 gallus gall
113	10	2.9	344	2	Q8RJD0	Q8rjd0 haemophilus	186	8	2.3	196	4	Q03399	Q03399 homo sapien
114	10	2.9	346	2	Q9S5J9	Q9s5j9 actinobacil	187	8	2.3	202	5	Q9VST6	Q9vst6 drosophila
115	10	2.9	346	2	Q51841	Q51841 actinobacil	188	8	2.3	202	10	Q9AY46	Q9ay46 oryza sativ
116	10	2.9	378	2	Q9RQ28	Q9rq28 pasteurella	189	8	2.3	208	16	Q9ABR4	Q9abr4 caulobacter
117	9	2.6	146	2	Q930Q2	Q93qq2 brenneria l	190	8	2.3	214	2	Q93M22	Q93m22 streptomyce
118	9	2.6	146	2	Q930Q1	Q93qq1 brenneria q	191	8	2.3	216	16	Q9AAT5	Q9aat5 caulobacter
119	9	2.6	146	2	Q930Q0	Q93qq0 brenneria q	192	8	2.3	221	16	Q8XY00	Q8xy00 raiatonia s
120	9	2.6	146	2	Q930P9	Q93qp9 brenneria q	193	8	2.3	225	2	Q9L591	Q9l591 streptococc
121	9	2.6	146	2	Q930P8	Q93qp8 brenneria q	194	8	2.3	226	10	Q948H7	Q948h7 oryza sativ
122	9	2.6	146	2	Q930P7	Q93qp7 brenneria r	195	8	2.3	227	5	Q95XQ6	Q95xq6 caenorhabdi
123	9	2.6	148	2	Q930Q8	Q93qq8 brenneria r	196	8	2.3	227	16	Q06556	Q06556 mycobacteri
124	9	2.6	187	16	P74534	P74534 synchocyst	197	8	2.3	230	16	Q8YK55	Q8yk55 mycobacteri
125	9	2.6	191	13	Q9IB30	Q9ib30 cypselurus	198	8	2.3	235	12	Q91L37	Q91l37 sugarcane y
126	9	2.6	192	13	Q9IB27	Q9ib27 trachurus t	199	8	2.3	240	16	Q9RSN5	Q9rsn5 deinococcus
127	9	2.6	193	13	Q9IB33	Q9ib33 pennahia ar	200	8	2.3	241	3	Q9P3A6	Q9p3a6 neurospora
128	9	2.6	193	13	Q90331	Q90331 cyprinus ca	201	8	2.3	249	16	Q9L127	Q9l127 streptomyce
129	9	2.6	193	13	Q90332	Q90332 cyprinus ca	202	8	2.3	254	10	Q8VZA7	Q8vza7 arabidopsis
130	9	2.6	194	13	Q90W52	Q90w52 catanx deli	203	8	2.3	254	10	Q8S781	Q8s781 arabidopsis
131	9	2.6	194	13	Q90W44	Q90w44 decapteris	204	8	2.3	260	11	Q35455	Q35455 mus musculu
132	9	2.6	197	13	Q90W46	Q90w46 decapteris	205	8	2.3	262	10	Q8W2Q2	Q8w2q2 oryza sativ
133	9	2.6	198	13	Q9IB39	Q9ib39 thunnus thy	206	8	2.3	269	10	Q8S1F2	Q8s1f2 oryza sativ
134	9	2.6	198	13	Q9IB36	Q9ib36 katusonug	207	8	2.3	283	4	Q9UKC7	Q9ukc7 homo sapien
135	9	2.6	198	13	Q90W41	Q90w41 scomber jap	208	8	2.3	283	4	Q9Y417	Q9y417 homo sapien
136	9	2.6	203	13	Q12966	Q12966 fugu rubrip	209	8	2.3	285	5	Q8SXU6	Q8sxu6 drosophila
137	9	2.6	215	10	Q43719	Q43719 lycopersico	210	8	2.3	285	10	Q9AHY1	Q9ahy1 oryza sativ
138	9	2.6	249	2	Q9L575	Q9l575 streptococc	211	8	2.3	286	16	Q9EMH8	Q9emh8 streptomyce
139	9	2.6	310	5	Q9W496	Q9w496 drosophila	212	8	2.3	288	16	Q95563	Q95563 closterium
140	9	2.6	326	2	Q9X4S0	Q9x4s0 pseudomonas	213	8	2.3	289	10	Q39563	Q39563 mus musculu
141	9	2.6	330	2	Q44299	Q44299 aeromonas s	214	8	2.3	304	11	Q9D990	Q9d990 oryza sativ
142	9	2.6	344	2	Q9LA97	Q9la97 aeromonas h	215	8	2.3	308	10	Q8SB66	Q8sb66 oryza sativ
143	9	2.6	361	10	Q9ZTY0	Q9zty0 emiliania h	216	8	2.3	311	4	Q96RX7	Q96rx7 homo sapien
144	9	2.6	403	2	P96773	P96773 haemophilus	217	8	2.3	319	2	Q9FIV0	Q9fiv0 flavobacte
145	9	2.6	407	2	P96774	P96774 haemophilus	218	8	2.3	321	2	Q93HK0	Q93hk0 streptomyce
146	9	2.6	424	10	Q9FM65	Q9fm65 arabidopsis	219	8	2.3	325	10	Q925X6	Q925x6 frankia sp.
147	9	2.6	443	5	Q76153	Q76153 periplaneta	220	8	2.3	325	10	Q8SB65	Q8sb65 oryza sativ
148	9	2.6	537	2	Q46977	Q46977 escherichia	221	8	2.3	326	5	Q9NFX5	Q9nf5 ceratitidis c
149	9	2.6	537	16	Q989A5	Q989a5 rhizobium l	222	8	2.3	326	5	Q62010	Q62010 ceratitidis c
150	9	2.6	581	5	Q20517	Q20517 caenorhabdi	223	8	2.3	327	10	Q94GU0	Q94gu0 oryza sativ
151	9	2.6	594	4	Q14772	Q14772 homo sapien	224	8	2.3	332	5	Q9NFX7	Q9nf7 ceratitidis c
152	9	2.6	706	5	Q9VVR5	Q9vyr5 drosophila	225	8	2.3	332	12	Q91GY8	Q91gy8 orf virus.
153	9	2.6	803	2	Q9RF11	Q9rf11 myxococcus	226	8	2.3	332	12	Q91GY8	Q91gy8 orf virus.
154	9	2.6	1013	5	Q9VVT7	Q9vyt7 drosophila	227	8	2.3	334	12	Q91GY9	Q91gy9 orf virus.
155	9	2.6	1061	16	Q8X8J5	Q8x8j5 escherichia	228	8	2.3	340	12	Q91GZ0	Q91gz0 orf virus.
156	9	2.6	1453	4	Q9Y6T1	Q9y6t1 homo sapien	229	8	2.3	340	12	Q910T9	Q910t9 orf virus.
157	9	2.6	1606	11	Q924A2	Q924a2 mus musculu	230	8	2.3	344	11	Q89037	Q89037 rattus norv
158	9	2.6	1608	4	Q96RK0	Q96rk0 homo sapien	231	8	2.3	346	4	Q9NSQ9	Q9nsg9 homo sapien
159	9	2.6	1785	5	Q25685	Q25685 plasmodium	232	8	2.3	348	2	Q8VPL3	Q8vpl3 pasteurella
160	9	2.6	2163	5	Q9NFB6	Q9nfb6 plasmodium	233	8	2.3	353	16	Q9CMN1	Q9cmn1 pasteurella
161	8	2.3	15	2	Q9R564	Q9r564 escherichia	234	8	2.3	354	1	Q9VMZ5	Q9vmz5 drosophila
162	8	2.3	90	5	Q9VV28	Q9vv28 drosophila	235	8	2.3	356	11	Q99L93	Q99l93 mus musculu

236 8 2.3 359 10 Q8RXA9  
 237 8 2.3 360 2 Q86254  
 238 8 2.3 361 12 Q9NMR9  
 239 8 2.3 362 10 Q9LWE1  
 240 8 2.3 363 10 Q9P837  
 241 8 2.3 364 10 Q8S9W0  
 242 8 2.3 365 10 Q9SF49  
 243 8 2.3 366 10 Q03991  
 244 8 2.3 367 4 Q96Q15  
 245 8 2.3 368 5 Q9V105  
 246 8 2.3 369 2 Q9LAY6  
 247 8 2.3 370 2 Q9LAY1  
 248 8 2.3 371 2 Q9LAY2  
 249 8 2.3 372 16 Q8XAP7  
 250 8 2.3 373 2 Q9LAY0  
 251 8 2.3 374 16 Q9FC63  
 252 8 2.3 375 2 Q9LAY5  
 253 8 2.3 376 2 Q9LAY4  
 254 8 2.3 377 16 Q9A2W5  
 255 8 2.3 378 10 Q9PWF7  
 256 8 2.3 379 10 Q9PWF7  
 257 8 2.3 380 5 Q20198  
 258 8 2.3 381 6 Q8X053  
 259 8 2.3 382 6 Q8BE23  
 260 8 2.3 383 10 Q8S5P0  
 261 8 2.3 384 11 Q03592  
 262 8 2.3 385 3 Q9UVD1  
 263 8 2.3 386 16 Q9RT74  
 264 8 2.3 387 2 Q9P8A6  
 265 8 2.3 388 4 Q9H5W9  
 266 8 2.3 389 12 Q9IC9H  
 267 8 2.3 390 10 Q96343  
 268 8 2.3 391 16 Q8X205  
 269 8 2.3 392 5 Q8T0S2  
 270 8 2.3 393 10 Q8W204  
 271 8 2.3 394 5 Q9W0N9  
 272 8 2.3 395 16 Q9AAQ8  
 273 8 2.3 396 16 Q9AAZ3  
 274 8 2.3 397 16 Q9S2Q5  
 275 8 2.3 398 16 Q9RSC6  
 276 8 2.3 399 16 Q9HY28  
 277 8 2.3 400 16 Q9L1P6  
 278 8 2.3 401 2 Q9L1P6  
 279 8 2.3 402 2 Q9L1P6  
 280 8 2.3 403 10 Q23831  
 281 8 2.3 404 10 Q9SSV0  
 282 8 2.3 405 10 Q9SXH0  
 283 8 2.3 406 10 Q9M5W9  
 284 8 2.3 407 2 Q9KK28  
 285 8 2.3 408 11 Q9R1D9  
 286 8 2.3 409 16 Q9XAR9  
 287 8 2.3 410 5 Q9GRF0  
 288 8 2.3 411 16 Q83619  
 289 8 2.3 412 16 Q83619  
 290 8 2.3 413 16 Q83619  
 291 8 2.3 414 11 Q9WVF3  
 292 8 2.3 415 2 Q9R074  
 293 8 2.3 416 3 Q8C2N3  
 294 8 2.3 417 5 Q9XU12  
 295 8 2.3 418 12 Q65820  
 296 8 2.3 419 16 Q9RKL5  
 297 8 2.3 420 5 Q9VZB8  
 298 8 2.3 421 8 Q9VZB8  
 299 8 2.3 422 11 Q9WVF4  
 300 8 2.3 423 8 Q9R071  
 301 8 2.3 424 7 Q8SNA3  
 302 8 2.3 425 5 Q9NDF9  
 303 8 2.3 426 2 Q9F2B0  
 304 8 2.3 427 5 Q95TX9  
 305 8 2.3 428 3 Q43024  
 306 8 2.3 429 3 Q9HE23  
 307 8 2.3 430 10 Q9L174  
 308 8 2.3 431 5 Q9VTF0  
 309 8 2.3 432 4 Q92502

Q8RXA9 zea mays (m  
 Q86254 haemophilus  
 Q9NMR9 lymantria d  
 Q9LWE1 oryza sativ  
 Q9P837 candida alb  
 Q8S9W0 oryza sativ  
 Q9SF49 arabidopsis  
 Q03991 daucus caro  
 Q96Q15 homo sapien  
 Q9V105 drosophila  
 Q9LAY6 streptococ  
 Q9LAY1 streptococ  
 Q9LAY2 streptococ  
 Q8XAP7 escherichia  
 Q9LAY0 streptococ  
 Q9FC63 streptococ  
 Q9LAY5 streptococ  
 Q9LAY4 streptococ  
 Q9A2W5 caulobacter  
 Q9PWF7 oryza sativ  
 Q9PWF7 avena fatua  
 Q20198 caenorhabdi  
 Q8X053 neurospora  
 Q8BE23 macaca fasc  
 Q8S5P0 oryza sativ  
 Q03592 mus musculu  
 Q9UVD1 pneumocysti  
 Q9RT74 deinothococcus  
 Q9P8A6 treponema p  
 Q9H5W9 homo sapien  
 Q9IC9H macropodid  
 Q96343 brassica na  
 Q8X205 ralstonia s  
 Q8T0S2 drosophila  
 Q8W204 oryza sativ  
 Q9W0N9 drosophila  
 Q9AAQ8 caulobacter  
 Q9AAZ3 caulobacter  
 Q9S2Q5 streptomyce  
 Q9RSC6 deinothococcus  
 Q9HY28 pseudomonas  
 Q9L1P6 streptomyce  
 Q9L1P6 streptomyce  
 Q23831 arabidopsis  
 Q9SSV0 arabidopsis  
 Q9SXH0 arabidopsis  
 Q9M5W9 arabidopsis  
 Q9KK28 streptococ  
 Q9R1D9 mus musculu  
 Q9XAR9 streptomyce  
 Q9GRF0 caenorhabdi  
 P72539 treponema p  
 Q83619 streptomyce  
 Q9WVF3 mus musculu  
 Q9R074 streptococ  
 Q9C2N3 neurospora  
 Q9XU12 caenorhabdi  
 Q65820 bovine heip  
 Q93107 acanthamoeb  
 Q9RKL5 streptomyce  
 Q9VZB8 drosophila  
 Q9WVF4 mus musculu  
 Q9R071 streptococ  
 Q8SNA3 mus musculu  
 Q9NDF9 balanus amp  
 Q9F2B0 thibacillu  
 Q95TX9 drosophila  
 Q43024 schizosacch  
 Q9HE23 neurospora  
 Q9L174 arabidopsis  
 Q9VTF0 drosophila  
 Q92502 homo sapien

309 8 2.3 1046 4 Q9P2X1  
 310 8 2.3 1056 10 Q9FW41  
 311 8 2.3 1088 4 Q9NRM7  
 312 8 2.3 1097 5 Q9U2T9  
 313 8 2.3 1098 11 Q9WTN8  
 314 8 2.3 1151 13 Q57580  
 315 8 2.3 1154 11 Q921R2  
 316 8 2.3 1360 3 Q9P422  
 317 8 2.3 1461 5 Q8T9F6  
 318 8 2.3 1474 5 Q8T4M0  
 319 8 2.3 1500 5 Q8T4L8  
 320 8 2.3 1503 5 Q8T4L8  
 321 8 2.3 1509 5 Q9SP10  
 322 8 2.3 1513 5 Q17970  
 323 8 2.3 1553 5 Q9STR0  
 324 8 2.3 1584 5 Q9J791  
 325 8 2.3 1676 3 Q8TG36  
 326 8 2.3 1678 11 Q924C5  
 327 8 2.3 1698 5 Q9V5J8  
 328 8 2.3 1785 10 Q8S789  
 329 8 2.3 2110 5 Q9VRA6  
 330 8 2.3 2197 5 Q9G296  
 331 8 2.3 3634 2 Q9JP78  
 332 8 2.3 6889 16 Q8XS40  
 333 8 2.3 10917 2 Q93NW6  
 334 7 2.0 45 9 Q8W701  
 335 7 2.0 63 2 Q9F212  
 336 7 2.0 70 10 Q8S0T1  
 337 7 2.0 83 5 Q9W6V8  
 338 7 2.0 94 9 Q8W6V8  
 339 7 2.0 102 12 Q9PXP5  
 340 7 2.0 102 12 Q9PXP4  
 341 7 2.0 108 17 Q9Y9N3  
 342 7 2.0 113 10 Q945Q3  
 343 7 2.0 113 17 Q97222  
 344 7 2.0 118 16 Q8XZ20  
 345 7 2.0 120 16 Q8XZ20  
 346 7 2.0 121 6 Q9BDC2  
 347 7 2.0 127 5 Q9SRA0  
 348 7 2.0 129 10 Q40615  
 349 7 2.0 132 10 Q9SE04  
 350 7 2.0 139 10 Q9ZT17  
 351 7 2.0 139 10 Q8R2R5  
 352 7 2.0 143 4 Q9H4U5  
 353 7 2.0 144 17 Q8U303  
 354 7 2.0 145 2 Q9ZAA7  
 355 7 2.0 147 2 Q97907  
 356 7 2.0 155 12 Q8QNK4  
 357 7 2.0 156 16 Q8XSU0  
 358 7 2.0 160 4 Q8TCG9  
 359 7 2.0 163 13 Q90W43  
 360 7 2.0 166 5 Q95Z68  
 361 7 2.0 171 10 Q9C684  
 362 7 2.0 171 13 Q9IB38  
 363 7 2.0 176 11 Q9D367  
 364 7 2.0 180 10 Q9SHY3  
 365 7 2.0 181 5 Q8SWS3  
 366 7 2.0 187 2 Q9FA14  
 367 7 2.0 187 11 Q9ESU4  
 368 7 2.0 188 11 Q9D7T0  
 369 7 2.0 189 5 Q8S2D3  
 370 7 2.0 190 13 Q91792  
 371 7 2.0 193 2 Q70032  
 372 7 2.0 193 13 Q90WC7  
 373 7 2.0 194 2 Q9L5B5  
 374 7 2.0 194 13 Q90W49  
 375 7 2.0 197 16 Q9L0F1  
 376 7 2.0 200 10 Q9AX80  
 377 7 2.0 200 17 Q58477  
 378 7 2.0 204 3 Q13598  
 379 7 2.0 204 10 Q8S2Q1  
 380 7 2.0 206 10 Q9LVA5  
 381 7 2.0 207 10 Q82227

Q9P2X1 homo sapien  
 Q9FW41 oryza sativ  
 Q9NRM7 homo sapien  
 Q9U2T9 caenorhabdi  
 Q9WTN8 rattus norv  
 Q57580 gallus galli  
 Q921R2 mus musculu  
 Q9P422 neurospora  
 Q8T9F6 drosophila  
 Q8T4M0 drosophila  
 Q9VLQ8 drosophila  
 Q8T4L8 drosophila  
 Q95P10 drosophila  
 Q17970 caenorhabdi  
 Q9STR0 drosophila  
 Q9J791 caenorhabdi  
 Q93791 caenorhabdi  
 Q8T9F6 ustilago ma  
 Q924C5 mus musculu  
 Q9V5J8 drosophila  
 Q8S789 oryza sativ  
 Q9VRA6 drosophila  
 Q9G296 plasmodium  
 Q9JP78 bordetella  
 Q8XS40 ralstonia s  
 Q93NW6 streptomyce  
 Q8W701 cyanophaga  
 Q9F212 roseateles  
 Q8S0T1 oryza sativ  
 Q9W6V8 drosophila  
 Q8W6V8 cyanophaga  
 Q9PXP5 hepatitis c  
 Q9PXP4 hepatitis c  
 Q9Y9N3 aeropyrum p  
 Q945Q3 arabidopsis  
 Q97222 sulfobobus  
 Q8XZ20 ralstonia s  
 Q8XZ20 ralstonia s  
 Q9BDC2 listeria in  
 Q9SRA0 bos taurus  
 Q9SRA0 drosophila  
 Q40615 oryza sativ  
 Q9SE04 oryza sativ  
 Q9ZT17 arabidopsis  
 Q8R2R5 oryza sativ  
 Q9H4U5 homo sapien  
 Q8U303 pyrococcus  
 Q9ZAA7 acidaminoco  
 Q97907 rhodobacter  
 Q8QNK4 ectocarpus  
 Q8XSU0 ralstonia s  
 Q8TCG9 homo sapien  
 Q90W43 deceptorus  
 Q95Z68 osteria  
 Q9C684 arabidopsis  
 Q9IB38 thunnus thy  
 Q9D367 mus musculu  
 Q9SHY3 arabidopsis  
 Q8SWS3 drosophila  
 Q9FA14 streptomyce  
 Q9ESU4 mus musculu  
 Q9D7T0 mus musculu  
 Q8S2D3 drosophila  
 Q91792 xenopus lae  
 Q70032 streptomyce  
 Q90WC7 oncorhynch  
 Q9L5B5 streptococ  
 Q90W49 deceptorus  
 Q9L0F1 streptomyce  
 Q9AX80 oryza sativ  
 Q58477 pyrococcus  
 Q13598 schizosacch  
 Q8S2Q1 oryza sativ  
 Q9LVA5 arabidopsis  
 Q82227 arabidopsis



382	7	2.0	209	2	Q9L593	Q9L593 streptococc	455	7	2.0	318	17	Q8TRU1	Q8TRU1 methanosarc
383	7	2.0	209	10	Q9PRP2	Q9PRP2 arabisopsi	456	7	2.0	320	10	Q8S833	Q8S833 oryza sativ
384	7	2.0	210	16	Q8Z981	Q8Z981 salmonella	457	7	2.0	321	16	Q3L154	Q3L154 vibrio chol
385	7	2.0	211	12	Q9G9B7	Q9G9B7 culex nigri	458	7	2.0	323	11	Q9EQ24	Q9EQ24 rattus norv
386	7	2.0	211	12	Q9L909	Q9L909 culex nigri	459	7	2.0	323	11	Q9EQ22	Q9EQ22 rattus norv
387	7	2.0	212	10	Q9M2D8	Q9M2D8 arabisopsi	460	7	2.0	325	2	Q3X4R7	Q3X4R7 pseudomonas
388	7	2.0	212	12	Q4L1980	Q4L1980 murid herpe	461	7	2.0	325	2	Q9X4R8	Q9X4R8 pseudomonas
389	7	2.0	212	16	Q92KL1	Q92KL1 rhizobium m	462	7	2.0	327	10	Q9FW19	Q9FW19 oryza sativ
390	7	2.0	213	10	Q43600	Q43600 oryza sativ	463	7	2.0	328	3	Q9UR34	Q9UR34 schizosacch
391	7	2.0	215	4	Q9UNGO	Q9UNGO homo sapien	464	7	2.0	329	11	Q9JK33	Q9JK33 mus musculu
392	7	2.0	222	2	Q9L584	Q9L584 streptococc	465	7	2.0	331	4	Q16509	Q16509 homo sapien
393	7	2.0	222	10	Q9S740	Q9S740 arabisopsi	466	7	2.0	331	5	Q9V728	Q9V728 drosophila
394	7	2.0	223	5	Q9VV16	Q9VV16 drosophila	467	7	2.0	333	4	Q9NY94	Q9NY94 homo sapien
395	7	2.0	228	5	Q17275	Q17275 brugia paha	468	7	2.0	335	5	Q8S254	Q8S254 drosophila
396	7	2.0	228	10	Q8S0R0	Q8S0R0 oryza sativ	469	7	2.0	338	10	Q9S7K6	Q9S7K6 oryza sativ
397	7	2.0	231	5	Q9VXE4	Q9VXE4 drosophila	470	7	2.0	339	11	Q8RJ30	Q8RJ30 mus musculu
398	7	2.0	233	2	Q9L568	Q9L568 streptococc	471	7	2.0	345	4	Q96IH2	Q96IH2 homo sapien
399	7	2.0	236	2	Q9L569	Q9L569 streptococc	472	7	2.0	347	16	Q9RR94	Q9RR94 delinococcus
400	7	2.0	236	12	Q8S028	Q8S028 pseudorabie	473	7	2.0	348	16	Q9RTK5	Q9RTK5 delinococcus
401	7	2.0	236	16	Q92BG4	Q92BG4 listeria in	474	7	2.0	349	11	Q9ERM9	Q9ERM9 mus musculu
402	7	2.0	238	16	Q990Q6	Q990Q6 streptomyce	475	7	2.0	350	10	Q9FM99	Q9FM99 arabisopsi
403	7	2.0	239	10	Q94EG7	Q94EG7 arabisopsi	476	7	2.0	351	2	Q93TD8	Q93TD8 pseudomonas
404	7	2.0	242	2	Q9L562	Q9L562 streptococc	477	7	2.0	351	5	Q8SZ25	Q8SZ25 drosophila
405	7	2.0	242	10	Q8RF1	Q8RF1 oryza sativ	478	7	2.0	354	5	Q9VCN5	Q9VCN5 drosophila
406	7	2.0	243	2	Q9L567	Q9L567 streptococc	479	7	2.0	354	10	Q9ATT2	Q9ATT2 phacelurus
407	7	2.0	243	2	Q9L564	Q9L564 streptococc	480	7	2.0	354	16	Q8Z4E3	Q8Z4E3 salmonella
408	7	2.0	244	2	Q9L565	Q9L565 streptococc	481	7	2.0	355	10	Q9LE25	Q9LE25 chlamydomon
409	7	2.0	246	2	Q9L5B4	Q9L5B4 streptococc	482	7	2.0	356	16	Q8YAY7	Q8YAY7 bruceella me
410	7	2.0	246	2	Q9L578	Q9L578 streptococc	483	7	2.0	356	17	Q8TG22	Q8TG22 methanopyru
411	7	2.0	246	10	Q9LVW8	Q9LVW8 arabisopsi	484	7	2.0	362	10	Q9ATS8	Q9ATS8 cymbopogon
412	7	2.0	247	2	Q9L566	Q9L566 streptococc	485	7	2.0	362	12	Q04325	Q04325 chicory yel
413	7	2.0	249	2	Q9L585	Q9L585 streptococc	486	7	2.0	365	16	Q9RUH9	Q9RUH9 delinococcus
414	7	2.0	249	2	Q9L570	Q9L570 streptococc	487	7	2.0	366	10	Q94339	Q94339 arabisopsi
415	7	2.0	249	5	Q8TA41	Q8TA41 heterodera	488	7	2.0	371	12	Q8V973	Q8V973 lilly mottle
416	7	2.0	249	10	Q9FKJ8	Q9FKJ8 arabisopsi	489	7	2.0	374	2	Q9F0F7	Q9F0F7 campylobact
417	7	2.0	249	10	Q94J05	Q94J05 oryza sativ	490	7	2.0	375	16	Q9RW21	Q9RW21 delinococcus
418	7	2.0	249	16	Q98M22	Q98M22 rhizobium l	491	7	2.0	377	10	Q9FTN9	Q9FTN9 oryza sativ
419	7	2.0	251	16	Q98BC9	Q98BC9 rhizobium l	492	7	2.0	380	2	Q9S405	Q9S405 proteus mir
420	7	2.0	252	10	Q9S2U5	Q9S2U5 arabisopsi	493	7	2.0	380	11	Q9LWA6	Q9LWA6 mus musculu
421	7	2.0	254	2	Q9L563	Q9L563 streptococc	494	7	2.0	384	10	Q94DU1	Q94DU1 oryza sativ
422	7	2.0	255	2	Q9L5B6	Q9L5B6 streptococc	495	7	2.0	384	11	Q9D4D1	Q9D4D1 mus musculu
423	7	2.0	255	2	Q9L581	Q9L581 streptococc	496	7	2.0	388	5	Q9VMV9	Q9VMV9 drosophila
424	7	2.0	255	4	Q9H3S2	Q9H3S2 homo sapien	497	7	2.0	388	16	Q88027	Q88027 streptomyce
425	7	2.0	255	10	Q9LGM5	Q9LGM5 oryza sativ	498	7	2.0	390	5	Q9VAZ8	Q9VAZ8 drosophila
426	7	2.0	256	2	Q9L590	Q9L590 streptococc	499	7	2.0	393	17	Q9HJZ2	Q9HJZ2 thermoplasma
427	7	2.0	257	2	Q9L594	Q9L594 streptococc	500	7	2.0	393	2	Q9LAZ3	Q9LAZ3 streptococc
428	7	2.0	257	4	Q96J66	Q96J66 homo sapien	501	7	2.0	393	11	Q9J3F4	Q9J3F4 mus musculu
429	7	2.0	258	4	Q9BR67	Q9BR67 homo sapien	502	7	2.0	398	2	Q9RTM1	Q9RTM1 streptomyce
430	7	2.0	258	16	Q9K482	Q9K482 streptomyce	503	7	2.0	399	5	Q9VHA7	Q9VHA7 drosophila
431	7	2.0	259	16	Q92X87	Q92X87 rhizobium m	504	7	2.0	400	16	Q9ADJ6	Q9ADJ6 streptomyce
432	7	2.0	261	16	Q9JX72	Q9JX72 neisseria m	505	7	2.0	401	2	Q9LAZ2	Q9LAZ2 streptococc
433	7	2.0	262	16	Q9RTQ7	Q9RTQ7 delinococcus	506	7	2.0	404	10	Q9FGJ5	Q9FGJ5 arabisopsi
434	7	2.0	265	16	Q8YUV1	Q8YUV1 anabaena sp	507	7	2.0	404	12	Q9LF26	Q9LF26 cydia pomon
435	7	2.0	265	16	Q8UD55	Q8UD55 agrobacteri	508	7	2.0	405	16	Q92NK3	Q92NK3 rhizobium m
436	7	2.0	275	2	Q8RKD3	Q8RKD3 erwinia chr	509	7	2.0	407	10	Q9FRC8	Q9FRC8 oryza sativ
437	7	2.0	275	12	Q8V705	Q8V705 tulip band-	510	7	2.0	407	10	Q23555	Q23555 arabisopsi
438	7	2.0	278	12	Q83418	Q83418 pseudorabie	511	7	2.0	407	10	Q23555	Q23555 arabisopsi
439	7	2.0	278	16	Q9RL59	Q9RL59 streptomyce	512	7	2.0	409	3	Q8X0K2	Q8X0K2 neurospora
440	7	2.0	279	10	Q9CAS2	Q9CAS2 arabisopsi	513	7	2.0	412	2	P95595	P95595 rhodobacter
441	7	2.0	282	16	Q8XMR7	Q8XMR7 clostridium	514	7	2.0	413	2	Q56077	Q56077 streptomyce
442	7	2.0	283	16	Q8XXN3	Q8XXN3 ralstonia s	515	7	2.0	416	2	Q33481	Q33481 psychrobact
443	7	2.0	286	2	Q9R640	Q9R640 mycobacteri	516	7	2.0	425	4	Q9NPN3	Q9NPN3 homo sapien
444	7	2.0	289	10	Q41824	Q41824 zea mays (m	517	7	2.0	425	17	Q9HPW5	Q9HPW5 halobacteri
445	7	2.0	290	16	Q99QA0	Q99QA0 streptomyce	518	7	2.0	426	16	Q8UHH4	Q8UHH4 agrobacteri
446	7	2.0	294	10	Q8WQ08	Q8WQ08 sorghum bic	519	7	2.0	428	16	Q9RIP5	Q9RIP5 streptococc
447	7	2.0	296	5	Q9V729	Q9V729 drosophila	520	7	2.0	430	16	Q8YR44	Q8YR44 anabaena sp
448	7	2.0	296	16	Q87129	Q87129 pseudomonas	521	7	2.0	431	10	Q8VZ63	Q8VZ63 arabisopsi
449	7	2.0	297	10	Q41122	Q41122 phaseolus v	522	7	2.0	434	10	Q8RWB6	Q8RWB6 arabisopsi
450	7	2.0	305	16	Q8XUP6	Q8XUP6 ralstonia s	523	7	2.0	435	10	Q9SUW1	Q9SUW1 arabisopsi
451	7	2.0	307	16	Q8UDS6	Q8UDS6 agrobacteri	524	7	2.0	437	4	Q9G2Q2	Q9G2Q2 homo sapien
452	7	2.0	310	16	Q8Y2T9	Q8Y2T9 ralstonia s	525	7	2.0	437	10	Q9FDW2	Q9FDW2 oryza sativ
453	7	2.0	314	10	Q8S750	Q8S750 oryza sativ	526	7	2.0	442	10	Q9LWR6	Q9LWR6 oryza sativ
454	7	2.0	317	4	Q96B32	Q96B32 homo sapien	527	7	2.0	445	4	Q96FB6	Q96FB6 homo sapien

528	7	2.0	449	12	Q86537	Q86537 tulip break	601	7	2.0	642	12	Q65846
529	7	2.0	450	12	Q80N85	Q86n85 ectocarpus	602	7	2.0	643	5	Q9XUT0
530	7	2.0	451	3	Q08N85	Q08657 moraxella c	603	7	2.0	648	17	Q28883
531	7	2.0	455	5	Q61747	Q61747 caenorhabdi	604	7	2.0	649	16	Q9CKD9
532	7	2.0	457	16	Q12650	Q12650 streptococ	605	7	2.0	652	11	Q9D2M6
533	7	2.0	460	12	Q12659	Q12659 apple chlor	606	7	2.0	662	10	Q9LTX1
534	7	2.0	469	4	Q99492	Q99492 homo sapien	607	7	2.0	663	10	Q9FJ13
535	7	2.0	470	2	Q9K3D7	Q9K3D7 moritella s	608	7	2.0	674	10	Q9C7B4
536	7	2.0	475	5	Q9NGJ2	Q9NGJ2 drosophila	609	7	2.0	676	2	Q07365
537	7	2.0	475	5	Q9NGJ1	Q9NGJ1 drosophila	610	7	2.0	677	4	Q8TCL1
538	7	2.0	475	5	Q9NGJ0	Q9NGJ0 drosophila	611	7	2.0	683	4	Q8WV85
539	7	2.0	475	5	Q9NGR2	Q9NGR2 drosophila	612	7	2.0	691	5	Q19243
540	7	2.0	475	5	Q9NGE6	Q9NGE6 drosophila	613	7	2.0	700	16	Q9PFT1
541	7	2.0	477	5	Q9W2X5	Q9W2X5 drosophila	614	7	2.0	703	16	Q9PP16
542	7	2.0	479	2	Q9LAX2	Q9LAX2 streptococ	615	7	2.0	703	16	Q9PP16
543	7	2.0	480	2	Q9LAX3	Q9LAX3 streptococ	616	7	2.0	716	11	Q8R5F8
544	7	2.0	481	2	Q9LAX5	Q9LAX5 streptococ	617	7	2.0	723	4	Q8T5E8
545	7	2.0	486	16	Q86746	Q86746 streptomyce	618	7	2.0	723	16	Q8VIR7
546	7	2.0	487	16	Q8XRH4	Q8XRH4 ralstonia s	619	7	2.0	724	6	Q9MIND
547	7	2.0	489	10	Q9SS90	Q9SS90 arabidopsis	620	7	2.0	726	11	Q924S6
548	7	2.0	494	10	Q9A8I4	Q9A8I4 oryza sativ	621	7	2.0	729	16	Q69743
549	7	2.0	495	16	Q9KYE4	Q9KYE4 streptomyce	622	7	2.0	733	4	Q9BZQ1
550	7	2.0	502	2	Q9LAX8	Q9LAX8 streptococ	623	7	2.0	739	3	Q9P683
551	7	2.0	508	16	Q9F2X3	Q9F2X3 streptomyce	624	7	2.0	743	16	Q9L0S2
552	7	2.0	512	5	Q9VM14	Q9VM14 drosophila	625	7	2.0	745	4	Q9P2N8
553	7	2.0	513	3	Q9C1X4	Q9C1X4 schizosacch	626	7	2.0	757	16	Q98QH0
554	7	2.0	515	2	Q9L8T0	Q9L8T0 treponema p	627	7	2.0	757	17	Q8TIV7
555	7	2.0	516	2	Q9L8T3	Q9L8T3 treponema p	628	7	2.0	758	10	Q9C838
556	7	2.0	519	2	Q9KK20	Q9KK20 streptococ	629	7	2.0	759	12	Q8UYT2
557	7	2.0	524	12	Q83417	Q83417 pseudorabie	630	7	2.0	772	17	Q8U3U2
558	7	2.0	524	16	Q8YI00	Q8YI00 deinococcus	631	7	2.0	784	16	Q8XS28
559	7	2.0	526	12	Q95027	Q95027 pseudorabie	632	7	2.0	786	16	Q8XPV8
560	7	2.0	528	2	Q03536	Q03536 escherichia	633	7	2.0	787	3	Q94096
561	7	2.0	532	10	Q9FWD7	Q9FWD7 oryza sativ	634	7	2.0	801	5	Q93635
562	7	2.0	538	16	Q9R112	Q9R112 fusobacteri	635	7	2.0	809	16	Q8X224
563	7	2.0	540	12	Q9R371	Q9R371 cercopitheci	636	7	2.0	811	5	Q9VT40
564	7	2.0	541	16	Q9RDM9	Q9RDM9 streptomyce	637	7	2.0	811	16	Q9X8T0
565	7	2.0	547	10	Q94GC1	Q94GC1 oryza sativ	638	7	2.0	816	4	Q96G51
566	7	2.0	551	16	Q9HUB4	Q9HUB4 pseudomonas	639	7	2.0	824	4	Q8TEK9
567	7	2.0	556	5	Q95RC6	Q95RC6 drosophila	640	7	2.0	826	10	Q940X9
568	7	2.0	556	16	Q53678	Q53678 mycobacteri	641	7	2.0	833	16	Q8YU06
569	7	2.0	557	5	Q23933	Q23933 drosophila	642	7	2.0	845	5	Q9GRLL
570	7	2.0	566	11	Q9ER03	Q9ER03 mus musculu	643	7	2.0	852	11	Q8R077
571	7	2.0	568	16	Q9RWU8	Q9RWU8 deinococcus	644	7	2.0	854	11	Q54971
572	7	2.0	569	6	Q28616	Q28616 ryptocollagus	645	7	2.0	855	4	Q8WTX5
573	7	2.0	570	2	Q9APH1	Q9APH1 leptospira	646	7	2.0	855	17	Q8TTP9
574	7	2.0	574	3	Q36027	Q36027 schizosacch	647	7	2.0	857	16	Q9P7E8
575	7	2.0	574	5	Q17411	Q17411 aedes aegypt	648	7	2.0	862	4	Q9BY75
576	7	2.0	574	16	Q9RTJ3	Q9RTJ3 deinococcus	649	7	2.0	870	3	Q8W2W3
577	7	2.0	576	5	Q9WX72	Q9WX72 drosophila	650	7	2.0	884	4	Q00302
578	7	2.0	580	4	Q96ID0	Q96ID0 homo sapien	651	7	2.0	884	4	Q8MU30
579	7	2.0	584	16	Q9FCJ3	Q9FCJ3 streptomyce	652	7	2.0	903	4	Q96F66
580	7	2.0	586	10	Q40643	Q40643 oryza sativ	653	7	2.0	907	16	Q8Y260
581	7	2.0	586	16	Q9L0T7	Q9L0T7 streptomyce	654	7	2.0	913	16	Q8UJ51
582	7	2.0	587	10	Q23241	Q23241 arabidopsis	655	7	2.0	923	6	Q97745
583	7	2.0	587	16	Q9HUC8	Q9HUC8 pseudomonas	656	7	2.0	932	5	Q01623
584	7	2.0	587	16	Q9F4K5	Q9F4K5 caulobacter	657	7	2.0	934	4	Q9P2B0
585	7	2.0	588	10	Q948Y3	Q948Y3 oryza sativ	658	7	2.0	938	3	Q96V14
586	7	2.0	589	4	Q75148	Q75148 homo sapien	659	7	2.0	942	5	Q8WRX5
587	7	2.0	590	5	Q8SSB8	Q8SSB8 encephalito	660	7	2.0	945	6	Q77589
588	7	2.0	594	2	Q9V099	Q9V099 alcaligenes	661	7	2.0	948	6	Q9T7D7
589	7	2.0	594	5	Q9VEP4	Q9VEP4 drosophila	662	7	2.0	954	5	Q95X23
590	7	2.0	596	4	Q9NXH0	Q9NXH0 homo sapien	663	7	2.0	954	13	Q91909
591	7	2.0	596	4	Q96BB7	Q96BB7 homo sapien	664	7	2.0	964	6	Q97744
592	7	2.0	596	11	Q9CVF3	Q9CVF3 mus musculu	665	7	2.0	964	6	Q9TQ01
593	7	2.0	600	16	Q8Y088	Q8Y088 ralstonia s	666	7	2.0	964	6	Q9TQ00
594	7	2.0	606	4	Q9NP00	Q9NP00 homo sapien	667	7	2.0	972	4	Q99662
595	7	2.0	622	12	Q8V972	Q8V972 lily mottle	668	7	2.0	974	2	Q9S0V6
596	7	2.0	626	3	Q9HFW3	Q9HFW3 ashbya goss	669	7	2.0	974	11	Q63702
597	7	2.0	629	2	Q9K3D6	Q9K3D6 moritella s	670	7	2.0	974	13	Q985U3
598	7	2.0	629	6	Q29426	Q29426 ryptocollagus	671	7	2.0	975	13	P79750
599	7	2.0	636	16	Q8U9F8	Q8U9F8 agrobacteri	672	7	2.0	977	13	Q918N6
600	7	2.0	640	16	Q06293	Q06293 mycobacteri	673	7	2.0			

Q65846 barley yell  
Q9xut0 caenorhabdi  
Q28883 archaeglob  
Q9ckd9 pasteurella  
Q9d2m6 mus musculu  
Q9ltx1 arabidopsis  
Q9fj13 arabidopsis  
Q9c7b4 arabidopsis  
Q07365 chlamydia t  
Q8tcl1 homo sapien  
Q8wv85 homo sapien  
Q19243 caenorhabdi  
Q9pft1 xylella fas  
Q9pp16 campylobact  
Q8f5f8 mus musculu  
Q8t668 homo sapien  
Q8vir7 mycobacteri  
Q9myn0 bos taurus  
Q92496 mus musculu  
Q96743 mycobacteri  
Q9bzq1 homo sapien  
Q9p683 neurospora  
Q91092 streptomyce  
Q9p2n8 homo sapien  
Q8qho0 mycoplasma  
Q8t1v7 methanosarc  
Q8y828 arabidopsis  
Q8uyt2 lily mottle  
Q8u3u2 pyrococcus  
Q8xs28 ralstonia s  
Q8xp88 ralstonia s  
Q94096 pneumococci  
Q23635 caenorhabdi  
Q8v140 drosophila  
Q9x810 streptomyce  
Q96g51 homo sapien  
Q8cek9 homo sapien  
Q940x9 arabidopsis  
Q8yur6 anabaena sp  
Q9gr11 leishmania  
Q8r077 mus musculu  
Q54971 mus musculu  
Q8wtx5 homo sapien  
Q8tt99 methanosarc  
Q9p7e8 schizosacch  
Q98lk2 rhizobium l  
Q8by75 homo sapien  
Q8wz3 neurospora  
Q00302 homo sapien  
Q8wu30 homo sapien  
Q96f66 homo sapien  
Q8y260 anabaena sp  
Q8u551 agrobacteri  
Q97745 sus scrofa  
Q969v6 homo sapien  
Q01623 caenorhabdi  
Q9p2b0 homo sapien  
Q96v14 pneumococci  
Q8wrx5 anopheles g  
Q77589 equus cabal  
Q9tt47 trichosurus  
Q95x23 leishmania  
Q91909 xenopus lae  
Q97744 sus scrofa  
Q9tq01 sus scrofa  
Q9tq00 sus scrofa  
Q99662 homo sapien  
Q9s0v6 streptomyce  
Q63702 rattus ratt  
Q985u3 danio dangi  
P79750 fugu rubrip  
Q918n6 brachydanio

674	7	2.0	977	13	Q98SU4	Q98su4 danio alb	747	6	1.7	66	11	Q91WH0	Q91wh0 mus musculu
675	7	2.0	977	13	Q98SU1	Q98su1 danio nigro	748	6	1.7	67	10	Q87549	Q87549 bacillus ps
676	7	2.0	978	6	Q9XS93	Q9xs93 canis fami	749	6	1.7	67	10	Q85344	Q85344 capsicum an
677	7	2.0	978	11	Q63116	Q63116 rattus norv	750	6	1.7	67	16	Q9KDS3	Q9kds3 bacillus ha
678	7	2.0	979	6	Q8WN23	Q8wn23 canis fami	751	6	1.7	68	2	Q83015	Q83015 streptomyce
679	7	2.0	995	11	Q35615	Q35615 mus musculu	752	6	1.7	68	16	Q9K805	Q9k805 bacillus ha
680	7	2.0	1006	3	Q9C2M4	Q9c2m4 neurospora	753	6	1.7	69	8	Q31945	Q31945 cheno
681	7	2.0	1021	2	Q9K5L6	Q9k5l6 actinoplane	754	6	1.7	69	10	Q94D89	Q94d89 oryza sativ
682	7	2.0	1039	5	Q9VMG8	Q9vmg8 drosophila	755	6	1.7	70	5	Q16428	Q16428 caenorhabdi
683	7	2.0	1053	4	Q96KJ4	Q96kj4 homo sapien	756	6	1.7	70	16	Q98KA0	Q98ka0 rhizobium l
684	7	2.0	1087	5	Q26156	Q26156 plasmodium	757	6	1.7	72	5	Q9V5T4	Q9v5t4 drosophila
685	7	2.0	1095	5	Q9U4G4	Q9u4g4 drosophila	758	6	1.7	72	5	Q9V5T4	Q9v5t4 drosophila
686	7	2.0	1111	16	Q86522	Q86522 streptomyce	759	6	1.7	73	10	Q82337	Q82337 arabidopsis
687	7	2.0	1132	16	Q9RRC7	Q9rrc7 deinococcus	760	6	1.7	73	10	Q82337	Q82337 arabidopsis
688	7	2.0	1149	5	Q23315	Q23315 caenorhabdi	761	6	1.7	73	16	Q9PAD1	Q9pad1 xylella fas
689	7	2.0	1158	4	Q14113	Q14113 homo sapien	762	6	1.7	73	16	Q8XXV9	Q8xxv9 talstonia s
690	7	2.0	1172	5	Q9G210	Q9g210 caenorhabdi	763	6	1.7	74	12	Q9YJ88	Q9yj88 hepatitis c
691	7	2.0	1264	5	Q91767	Q91767 manduca sex	764	6	1.7	74	12	Q56576	Q56576 hepatitis c
692	7	2.0	1272	16	Q9FBR4	Q9fbr4 streptomyce	765	6	1.7	74	12	Q56578	Q56578 hepatitis c
693	7	2.0	1274	4	Q9UM53	Q9um53 homo sapien	766	6	1.7	74	12	Q56581	Q56581 hepatitis c
694	7	2.0	1312	4	Q9COC9	Q9coc9 homo sapien	767	6	1.7	74	12	Q56582	Q56582 hepatitis c
695	7	2.0	1313	4	Q9COC9	Q9coc9 homo sapien	768	6	1.7	74	12	Q81744	Q81744 hepatitis c
696	7	2.0	1343	4	Q9H7N4	Q9h7n4 homo sapien	769	6	1.7	74	12	Q81745	Q81745 hepatitis c
697	7	2.0	1406	4	Q9Y216	Q9y216 homo sapien	770	6	1.7	74	12	Q9YPO5	Q9ypo5 hepatitis c
698	7	2.0	1464	5	Q24132	Q24132 drosophila	771	6	1.7	74	12	Q9YPO4	Q9ypo4 hepatitis c
699	7	2.0	1464	5	Q23995	Q23995 drosophila	772	6	1.7	74	16	Q9PLV5	Q9plv5 campylobact
700	7	2.0	1464	5	Q9VC47	Q9vc47 drosophila	773	6	1.7	74	16	Q9PCA8	Q9pca8 xylella fas
701	7	2.0	1663	4	Q9UQ01	Q9uq01 homo sapien	774	6	1.7	74	17	Q97C53	Q97c53 thermoplas
702	7	2.0	1693	5	Q9W3P3	Q9w3p3 drosophila	775	6	1.7	75	5	Q62468	Q62468 caenorhabdi
703	7	2.0	1711	5	Q95YX3	Q95yx3 leishmania	776	6	1.7	75	5	Q9U3L6	Q9u3l6 caenorhabdi
704	7	2.0	1714	10	Q94HT9	Q94ht9 oryza sativ	777	6	1.7	77	5	Q9N822	Q9n822 trypanosoma
705	7	2.0	1766	5	Q25668	Q25668 plasmodium	778	6	1.7	77	16	Q8XX39	Q8xx39 talstonia s
706	7	2.0	1777	10	Q94HP9	Q94hp9 oryza sativ	779	6	1.7	79	2	Q8VM18	Q8vm18 pseudomonas
707	7	2.0	1819	10	Q8SAZ4	Q8saz4 oryza sativ	780	6	1.7	79	16	Q932N3	Q932n3 staphylococ
708	7	2.0	1883	4	Q96SC5	Q96sc5 homo sapien	781	6	1.7	79	16	Q8YEV8	Q8yev8 bruceella me
709	7	2.0	1905	4	Q96SC5	Q96sc5 homo sapien	782	6	1.7	80	2	Q84933	Q84933 streptococ
710	7	2.0	1929	3	Q95YQ9	Q95yq9 leishmania	783	6	1.7	80	2	Q93B65	Q93b65 salmonella
711	7	2.0	2146	3	Q95897	Q95897 aspergillus	784	6	1.7	82	2	Q93B28	Q93b28 salmonella
712	7	2.0	2146	3	Q60026	Q60026 aspergillus	785	6	1.7	82	2	Q933X5	Q933x5 salmonella
713	7	2.0	2209	5	Q97324	Q97324 plasmodium	786	6	1.7	82	16	Q9RSW2	Q9rsw2 deinococcus
714	7	2.0	2408	5	Q22184	Q22184 caenorhabdi	787	6	1.7	82	16	Q9JVM9	Q9jvm9 neisseria m
715	7	2.0	2592	3	Q9P3J0	Q9p3j0 neurospora	788	6	1.7	83	2	Q93AW8	Q93aw8 salmonella
716	7	2.0	2658	13	Q9QWFO	Q9qwf0 gallus gall	789	6	1.7	83	5	Q9VK56	Q9vks6 drosophila
717	7	2.0	3192	2	Q914W4	Q914w4 streptomyce	790	6	1.7	84	2	Q93B43	Q93b43 mycobacteri
718	7	2.0	3247	12	Q65593	Q65593 bovine herp	791	6	1.7	84	2	Q93B43	Q93b43 salmonella
719	7	2.0	3361	4	Q9Y556	Q9y556 homo sapien	792	6	1.7	84	2	Q93AY5	Q93ay5 salmonella
720	7	2.0	3369	5	Q9GUP2	Q9gup2 caenorhabdi	793	6	1.7	84	2	Q93AX8	Q93ax8 salmonella
721	7	2.0	3366	5	Q9VZ30	Q9vz30 drosophila	794	6	1.7	84	5	Q91899	Q91899 bombyx mori
722	7	2.0	3664	4	Q96T58	Q96t58 homo sapien	795	6	1.7	84	12	Q8V461	Q8v461 hepatitis c
723	7	2.0	5644	2	Q93NX8	Q93nx8 streptomyce	796	6	1.7	85	2	Q93B22	Q93b22 salmonella
724	7	2.0	5990	2	Q9RLP6	Q9rlp6 mycobacteri	797	6	1.7	85	2	Q93B12	Q93b12 salmonella
725	6	1.7	25	5	Q8T607	Q8t607 asterias ru	798	6	1.7	85	9	Q9MBR5	Q9mbr5 staphylococ
726	6	1.7	27	5	Q76527	Q76527 holothuria	799	6	1.7	86	16	Q8XTT4	Q8xtt4 clostridium
727	6	1.7	27	12	Q9Q988	Q9q988 hepatitis c	800	6	1.7	86	16	Q8XTT4	Q8xtt4 clostridium
728	6	1.7	35	16	Q9JV38	Q9jv38 neisseria m	801	6	1.7	87	5	Q9VQ08	Q9vq08 drosophila
729	6	1.7	40	2	Q49072	Q49072 mycoplasma	802	6	1.7	88	16	Q98CA3	Q98ga3 rhizobium l
730	6	1.7	43	4	Q14909	Q14909 homo sapien	803	6	1.7	89	5	Q9VBL4	Q9vbl4 drosophila
731	6	1.7	45	13	Q9DFK1	Q9dfk1 gillichthys	804	6	1.7	89	9	Q9ZXL4	Q9zxl4 bacterioph
732	6	1.7	48	16	Q8UE67	Q8ue67 agrobacteri	805	6	1.7	89	9	Q8SDV8	Q8sdv8 bacterioph
733	6	1.7	50	2	P81518	P81518 bacillus th	806	6	1.7	89	10	Q8ZPR9	Q8zpr9 arabidopsis
734	6	1.7	51	8	Q9XKE9	Q9xke9 grus japon	807	6	1.7	89	10	Q8S065	Q8s065 oryza sativ
735	6	1.7	53	16	Q8XVC5	Q8xvc5 talstonia s	808	6	1.7	90	2	Q93B20	Q93b20 salmonella
736	6	1.7	55	2	Q93B25	Q93b25 salmonella	809	6	1.7	90	2	Q93B18	Q93b18 salmonella
737	6	1.7	58	16	Q98DL6	Q98dl6 rhizobium l	810	6	1.7	90	16	Q9C6Y0	Q9c6y0 arabidopsis
738	6	1.7	58	16	Q9F238	Q9f238 streptomyce	811	6	1.7	90	16	Q9K2J6	Q9k2j6 vibrio chol
739	6	1.7	59	2	Q93B34	Q93b34 salmonella	812	6	1.7	91	10	Q9AWV1	Q9awv1 oryza sativ
740	6	1.7	61	10	Q8S955	Q8s955 oryza sativ	813	6	1.7	92	8	Q63073	Q63073 senecio vul
741	6	1.7	61	12	Q8VIC3	Q8vic3 hepatitis c	814	6	1.7	92	12	Q84848	Q84848 perina nuda
742	6	1.7	61	12	Q8VIC2	Q8vic2 hepatitis c	815	6	1.7	94	2	Q93B74	Q93b74 salmonella
743	6	1.7	62	12	Q8VIC0	Q8vic0 hepatitis c	816	6	1.7	94	2	Q93AY0	Q93ay0 salmonella
744	6	1.7	62	4	Q9PIA5	Q9pia5 homo sapien	817	6	1.7	94	16	Q828V8	Q828v8 salmonella
745	6	1.7	65	4	Q9Y2U1	Q9y2u1 homo sapien	818	6	1.7	96	10	Q8W394	Q8w394 oryza sativ
746	6	1.7	66	2	Q93AX5	Q93ax5 salmonella	819	6	1.7	97	2	Q93AV9	Q93av9 salmonella

820	1.7	97	10	Q9FTN1	Q9ftn1 oryza sativ	893	6	1.7	115	8	Q9MJJ4	Q9mj14 carabus gen
821	1.7	98	2	Q93B71	Q93b71 salmonella	894	6	1.7	115	8	Q9MJJ3	Q9mj13 carabus coa
822	1.7	98	2	Q93B10	Q93b10 salmonella	895	6	1.7	115	8	Q9MJJ2	Q9mj12 carabus abb
823	1.7	98	5	Q9VRG2	Q9vrg2 drosophila	896	6	1.7	115	8	Q9MJJ1	Q9mj11 carabus can
824	1.7	98	17	Q82WZ7	Q82wz7 pyrobaculum	897	6	1.7	115	8	Q9MJJ0	Q9mj10 carabus aur
825	1.7	99	2	Q68434	Q68434 leptospira	898	6	1.7	115	8	Q9MJJ9	Q9mj19 carabus arv
826	1.7	99	2	Q68436	Q68436 leptospira	899	6	1.7	115	16	Q8XHD6	Q8xhd6 clostridium
827	1.7	100	2	Q93B57	Q93b57 salmonella	900	6	1.7	115	16	Q8XGEO	Q8xge0 salmonella
828	1.7	100	2	Q93AV9	Q93av9 salmonella	901	6	1.7	116	2	Q93B23	Q93b23 salmonella
829	1.7	100	10	Q9SWS7	Q9sWS7 arabidopsis	902	6	1.7	116	8	Q21026	Q21026 carabus pia
830	1.7	101	2	Q93B44	Q93b44 salmonella	903	6	1.7	116	8	Q21022	Q21022 carabus mel
831	1.7	101	12	Q93IAN2	Q93ian2 hepatitis b	904	6	1.7	116	8	Q21835	Q21835 carabus rug
832	1.7	102	2	Q93AW5	Q93aw5 salmonella	905	6	1.7	116	8	Q21751	Q21751 carabus int
833	1.7	103	2	Q93B52	Q93b52 salmonella	906	6	1.7	116	8	Q21847	Q21847 carabus mel
834	1.7	103	2	Q93AV3	Q93av3 salmonella	907	6	1.7	116	10	Q94E04	Q94e04 oryza sativ
835	1.7	104	2	Q93PB6	Q93pb6 microscilla	908	6	1.7	117	11	Q9D2C1	Q9d2c1 mus musculus
836	1.7	104	2	Q93AZ9	Q93az9 salmonella	909	6	1.7	118	5	Q9NE05	Q9ne05 caenorhabdi
837	1.7	104	10	Q9LPV3	Q9lpv3 arabidopsis	910	6	1.7	118	16	Q8ZE70	Q8ze70 yersinia pe
838	1.7	104	16	Q8YR36	Q8yr36 anabaena sp	911	6	1.7	118	17	Q97Z66	Q97z66 sulfobus
839	1.7	104	17	Q9HL12	Q9hl12 thermoplas	912	6	1.7	119	12	Q67867	Q67867 hepatitis b
840	1.7	105	2	Q9AN17	Q9an17 bradyrhizob	913	6	1.7	119	12	Q91U87	Q91u87 hepatitis b
841	1.7	105	2	Q93B67	Q93b67 salmonella	914	6	1.7	119	12	Q91U86	Q91u86 hepatitis b
842	1.7	105	2	Q93B63	Q93b63 salmonella	915	6	1.7	119	12	Q91U85	Q91u85 hepatitis b
843	1.7	105	2	Q93B26	Q93b26 salmonella	916	6	1.7	119	16	Q8XAG6	Q8xag6 escherichia
844	1.7	105	2	Q93AX9	Q93ax9 salmonella	917	6	1.7	119	16	Q9L103	Q9l103 streptomyce
845	1.7	105	5	Q9N456	Q9n456 caenorhabdi	918	6	1.7	120	2	Q93AW2	Q93aw2 salmonella
846	1.7	106	8	Q9G744	Q9g744 convoluta c	919	6	1.7	120	3	Q14393	Q14393 schizosacch
847	1.7	107	2	Q93B73	Q93b73 salmonella	920	6	1.7	120	16	Q9RY81	Q9ry81 deinococcus
848	1.7	107	2	Q93B38	Q93b38 salmonella	921	6	1.7	121	2	Q93AV7	Q93av7 salmonella
849	1.7	107	2	Q932Q3	Q932q3 salmonella	922	6	1.7	121	10	Q9C8N8	Q9c8n8 arabidopsis
850	1.7	107	16	Q9ADC4	Q9adc4 streptomyce	923	6	1.7	122	5	Q9VVZ5	Q9vvz5 drosophila
851	1.7	108	2	Q93B78	Q93b78 salmonella	924	6	1.7	122	8	Q9MKM6	Q9mkM6 carabus abb
852	1.7	108	6	Q9XST8	Q9xst8 canis famil	925	6	1.7	122	8	Q9T279	Q9t279 carabus spl
853	1.7	108	10	Q9FVY4	Q9fvy4 oryza sativ	926	6	1.7	122	10	P93309	P93309 arabidopsis
854	1.7	108	10	Q94CY1	Q94cy1 oryza sativ	927	6	1.7	122	16	Q8XF39	Q8xf39 salmonella
855	1.7	108	16	Q99S54	Q99s54 staphylococ	928	6	1.7	123	2	Q93B70	Q93b70 salmonella
856	1.7	108	16	Q9CE28	Q9ce28 lactococcus	929	6	1.7	123	2	Q93AW9	Q93aw9 salmonella
857	1.7	109	2	Q93B61	Q93b61 salmonella	930	6	1.7	123	16	Q8ZJ17	Q8zj17 yersinia pe
858	1.7	109	5	Q9VV10	Q9vv10 drosophila	931	6	1.7	123	17	Q29448	Q29448 archaeoglob
859	1.7	109	10	Q8W5F8	Q8w5f8 oryza sativ	932	6	1.7	124	2	Q93SB7	Q93sb7 frankia sp.
860	1.7	109	12	Q81298	Q81298 hepatitis c	933	6	1.7	124	2	Q93GL2	Q93gl2 frankia sp.
861	1.7	109	12	Q81300	Q81300 hepatitis c	934	6	1.7	124	2	Q93B01	Q93b01 salmonella
862	1.7	109	12	Q81452	Q81452 hepatitis c	935	6	1.7	124	12	Q9QME9	Q9qme9 norwalk-lik
863	1.7	109	12	Q81459	Q81459 hepatitis c	936	6	1.7	124	16	Q9PG56	Q9pg56 xylella fas
864	1.7	109	12	Q81301	Q81301 hepatitis c	937	6	1.7	124	15	Q8R989	Q8r989 thermoanaer
865	1.7	109	12	Q81543	Q81543 hepatitis c	938	6	1.7	125	2	Q93M11	Q93m11 streptomyce
866	1.7	109	12	Q81482	Q81482 hepatitis c	939	6	1.7	125	2	Q93AZ7	Q93az7 salmonella
867	1.7	109	12	Q81545	Q81545 hepatitis c	940	6	1.7	125	2	Q93AZ4	Q93az4 salmonella
868	1.7	109	12	Q81802	Q81802 hepatitis c	941	6	1.7	125	12	Q91AP1	Q91ap1 hepatitis b
869	1.7	109	12	Q81804	Q81804 hepatitis c	942	6	1.7	125	12	Q91AP0	Q91ap0 hepatitis b
870	1.7	109	17	Q30024	Q30024 archaeoglob	943	6	1.7	125	12	Q91AN9	Q91an9 hepatitis b
871	1.7	110	2	Q93B55	Q93b55 salmonella	944	6	1.7	125	12	Q91AN7	Q91an7 hepatitis b
872	1.7	110	2	Q93B14	Q93b14 salmonella	945	6	1.7	125	12	Q91AN6	Q91an6 hepatitis b
873	1.7	110	2	Q933C1	Q933c1 salmonella	946	6	1.7	125	12	Q91AN5	Q91an5 hepatitis b
874	1.7	110	12	Q9DWK2	Q9dWk2 hepatitis c	947	6	1.7	125	12	Q91AN4	Q91an4 hepatitis b
875	1.7	111	2	Q93B77	Q93b77 salmonella	948	6	1.7	125	12	Q91AN3	Q91an3 hepatitis b
876	1.7	111	2	Q93B03	Q93b03 salmonella	949	6	1.7	125	12	Q91AN1	Q91an1 hepatitis b
877	1.7	111	8	Q9WJ17	Q9wj17 campalita m	950	6	1.7	125	12	Q91AN0	Q91an0 hepatitis b
878	1.7	111	12	Q67928	Q67928 hepatitis b	951	6	1.7	125	12	Q91AN9	Q91an9 hepatitis b
879	1.7	111	12	Q67940	Q67940 hepatitis b	952	6	1.7	125	16	Q9RRH9	Q9rrh9 deinococcus
880	1.7	111	12	Q67931	Q67931 hepatitis b	953	6	1.7	126	2	Q93B59	Q93b59 salmonella
881	1.7	112	2	Q93B42	Q93b42 salmonella	954	6	1.7	126	2	Q93B31	Q93b31 salmonella
882	1.7	112	2	Q93B00	Q93b00 salmonella	955	6	1.7	126	2	Q93B17	Q93b17 salmonella
883	1.7	113	10	Q92NXX2	Q92nx2 petunia hyb	956	6	1.7	126	2	Q93AZ3	Q93az3 salmonella
884	1.7	114	2	Q93B72	Q93b72 salmonella	957	6	1.7	126	10	Q9ZT18	Q9zt18 arabidopsis
885	1.7	114	2	Q93B13	Q93b13 salmonella	958	6	1.7	126	16	Q9FBX3	Q9fbx3 streptomyce
886	1.7	114	2	Q93AZ6	Q93az6 salmonella	959	6	1.7	127	2	Q54743	Q54743 streptococ
887	1.7	114	2	Q93AZ5	Q93az5 salmonella	960	6	1.7	127	2	Q93B79	Q93b79 salmonella
888	1.7	114	15	Q39132	Q39132 human immu	961	6	1.7	127	2	Q93B30	Q93b30 salmonella
889	1.7	115	2	Q93B27	Q93b27 salmonella	962	6	1.7	127	17	Q8ZSW8	Q8zsw8 pyrobaculum
890	1.7	115	2	Q93AY1	Q93ay1 salmonella	963	6	1.7	128	2	Q93AX0	Q93ax0 salmonella
891	1.7	115	8	Q9TK97	Q9tk97 kochia scop	964	6	1.7	128	10	Q9MAW0	Q9maw0 bruguliera g
892	1.7	115	8	Q9MJJ7	Q9mj17 carabus nit	965	6	1.7	128	10	Q9MAW0	Q9maw0 bruguliera g

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966 10 09L124
967 128 10 0943D8
968 128 10 0943D8
969 128 2 093B80
970 128 2 093B80
971 128 2 093B80
972 128 2 093B80
973 128 2 093B80
974 128 2 093B80
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1000 128 2 093B80

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## ALIGNMENTS

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RESULT 1
Q99114
ID Q99114 PRELIMINARY; PRT; 238 AA.
AC Q99114
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE Outer membrane protein A (Outer membrane protein II) (Fragment).
GN OMPA.
OS Escherichia vulneris.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29943;
RA MEDLINE=92065252; PubMed=1955870;
RT Lawrence J.G., Ochman H., Hartl D.L.;
RT "Molecular and evolutionary relationships among enteric bacteria.";
CC -1- SUBCELLULAR LOCATION: OUTER MEMBRANE.
DR EMBL; M63356; AAA24233.1;
DR HSP; P02934; IQJP.
DR InterPro; IPR001145; Bac_OmpA.
DR Pfam; PF00691; OmpA; 1.
DR PRINTS; PR01021; OmpA_membrane; 1.
DR PRODOM; PD000930; Bac_OmpA; 1.
DR PROSITE; PS01068; OmpA; 1.
KW Outer membrane; Porin; Phage recognition.
FT NON_TER 1
FT NON_TER 238
SQ SEQUENCE 238 AA; 25553 MW; BCD6AF25240202B CRC64;
Query Match 10.5%; Score 36; DB 2; Length 238;
Best Local Similarity 100.0%; Pred. No. 6e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 210 TKHFTLKSDVLFNFNFKATLKPEGQALDQLYTQLSN 245
Db 113 TKHFTLKSDVLFNFNFKATLKPEGQALDQLYTQLSN 148

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SQ SEQUENCE 238 AA; 25604 MW; B05D116C01DD9733 CRC64;
Query Match 15.4%; Score 53; DB 2; Length 238;
Best Local Similarity 100.0%; Pred. No. 3.3e-45;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 213 FTLKSDVLFNFNFKATLKPEGQALDQLYTQLSNMNDPKGSVVVGLYTDRIQSE 265
Db 116 FTLKSDVLFNFNFKATLKPEGQALDQLYTQLSNMNDPKGSVVVGLYTDRIQSE 168
RESULT 2
Q99123
ID Q99123 PRELIMINARY; PRT; 238 AA.
AC Q99123
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE Outer membrane protein A (Outer membrane protein II) (Fragment)
DE (Version 2).
GN OMPA.
OS Enterobacter aerogenes (Aerobacter aerogenes).
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Enterobacter.
OX NCBI_TaxID=548;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E482;
RA MEDLINE=92065252; PubMed=1955870;
RT Lawrence J.G., Ochman H., Hartl D.L.;
RT "Molecular and evolutionary relationships among enteric bacteria.";
CC -1- SUBCELLULAR LOCATION: OUTER MEMBRANE.
DR EMBL; M63356; AAA24807.1;
DR HSP; P02934; IQJP.
DR InterPro; IPR001145; Bac_OmpA.
DR Pfam; PF00691; OmpA; 1.
DR PRINTS; PR01021; OmpA_membrane; 1.
DR PRODOM; PD000930; Bac_OmpA; 1.
DR PROSITE; PS01068; OmpA; 1.
KW Outer membrane; Porin; Phage recognition.
FT NON_TER 1
FT NON_TER 238
SQ SEQUENCE 238 AA; 25553 MW; BCD6AF25240202B CRC64;
Query Match 10.5%; Score 36; DB 2; Length 238;
Best Local Similarity 100.0%; Pred. No. 6e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 210 TKHFTLKSDVLFNFNFKATLKPEGQALDQLYTQLSN 245
Db 113 TKHFTLKSDVLFNFNFKATLKPEGQALDQLYTQLSN 148
RESULT 3
Q93QP1
ID Q93QP1 PRELIMINARY; PRT; 148 AA.
AC Q93QP1
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE Major outer membrane protein (Fragment).
GN OMPA.
OS Erwinia persicina.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Erwinia.
OX NCBI_TaxID=55211;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=33998;
RA Brown E.W., Davis R.M., Gouk C., van der Zwet T.;

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\*Allelic diversity of the major outer membrane protein (OmpA) gene among necrogenic phytopathogenic species: Molecular evolutionary aspects of relatedness.\*;  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF220801: AAK68967.1; -  
 DR InterPro: IPR001145; Bac\_OmpA.  
 DR InterPro: IPR000498; OmpA\_tmem.  
 DR Pfam: PF00691; OmpA; 1.  
 DR Pfam: PF01389; OmpA\_membrane; 1.  
 DR ProDom: PD000930; Bac\_OmpA; 1.  
 FT NON\_TER 1 148  
 FT NON\_TER 148 148  
 SQ SEQUENCE 148 AA; 16041 MW; 4124208BD384FCC1 CRC64;

Query Match 9.6%; Score 33; DB 2; Length 148;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-25;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 213 FTLKSDVLFNFNFKATLKPEGQALDQYLTOLSN 245  
 DB 107 FTLKSDVLFNFNFKATLKPEGQALDQYLTOLSN 139

RESULT 4  
 Q9L618 PRELIMINARY; PRT; 246 AA.

AC Q9L618;  
 DT 01-OCT-2000 (TRENBLrel. 15, Created)  
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
 DE Outer membrane protein A (Fragment).  
 GN OMPA.  
 OS Shigella flexneri.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Shigella.  
 OX NCBI\_TaxID=623;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wang Y., Kim K.S.;  
 RT "Structural and functional roles of OmpA in stress survival and invasion of brain microvascular endothelial cells in Escherichia coli.";  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF224271; AAF37889.1; -  
 DR HSSP: P02934; IQJP.  
 DR InterPro: IPR001145; Bac\_OmpA.  
 DR InterPro: IPR000498; OmpA\_tmem.  
 DR Pfam: PF00691; OmpA; 1.  
 DR Pfam: PF01389; OmpA\_membrane; 1.  
 FT NON\_TER 246 246  
 SQ SEQUENCE 246 AA; 26371 MW; 56C6D6225E6F079F CRC64;

Query Match 9.6%; Score 33; DB 2; Length 246;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-25;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 87 KAQGVQLTAKLGYPITDLDIYTRLGGMVWRAD 119  
 DB 94 KAQGVQLTAKLGYPITDLDIYTRLGGMVWRAD 126

RESULT 5  
 Q47880 PRELIMINARY; PRT; 244 AA.

AC Q47880;  
 DT 01-NOV-1996 (TRENBLrel. 01, Created)  
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
 DE Outer membrane protein II (Fragment).  
 GN OMPA.  
 OS Escherichia vulneris.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.

OX NCBI\_TaxID=566;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-92065252; PubMed-1955870;  
 RA Lawrence J.G., Ochman H., Hartl D.L.;  
 RT "Molecular and evolutionary relationships among enteric bacteria.";  
 RL J. Gen. Microbiol. 137:1911-1921(1991).  
 DR EMBL: M63350; AAA24241.1; -  
 DR HSSP: P02934; IQJP.  
 DR InterPro: IPR001145; Bac\_OmpA.  
 DR InterPro: IPR000498; OmpA\_tmem.  
 DR Pfam: PF00691; OmpA; 1.  
 DR Pfam: PF01389; OmpA\_membrane; 1.  
 DR PRINTS: PR01021; OMPADOMAIN.  
 DR ProDom: PD000930; Bac\_OmpA; 1.  
 DR PROSITE: PS01068; OmpA; 1.  
 FT NON\_TER 1 244  
 FT NON\_TER 244 244  
 SQ SEQUENCE 244 AA; 26275 MW; C6D068A6A0916179 CRC64;

Query Match 8.4%; Score 29; DB 2; Length 244;  
 Best Local Similarity 100.0%; Pred. No. 7.9e-21;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 210 TKHFTLKSDVLFNFNFKATLKPEGQALDQ 238  
 DB 119 TKHFTLKSDVLFNFNFKATLKPEGQALDQ 147

RESULT 6  
 Q99115 PRELIMINARY; PRT; 244 AA.

AC Q99115;  
 DT 01-NOV-1996 (TRENBLrel. 01, Created)  
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
 DE Outer membrane protein A (Outer membrane protein II) (Fragment).  
 GN OMPA.  
 OS Escherichia vulneris.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 OX NCBI\_TaxID=566;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ATCC 33821, AND ATCC 33822;  
 RX MEDLINE-92065252; PubMed-1955870;  
 RA Lawrence J.G., Ochman H., Hartl D.L.;  
 RT "Molecular and evolutionary relationships among enteric bacteria.";  
 RL J. Gen. Microbiol. 137:1911-1921(1991).  
 CC -1- SUBCELLULAR LOCATION: OUTER MEMBRANE.  
 DR EMBL: M63349; AAA24237.1; -  
 DR HSSP: P02934; IQJP.  
 DR InterPro: IPR001145; Bac\_OmpA.  
 DR InterPro: IPR000498; OmpA\_tmem.  
 DR Pfam: PF00691; OmpA; 1.  
 DR Pfam: PF01389; OmpA\_membrane; 1.  
 DR PRINTS: PR01021; OMPADOMAIN.  
 DR ProDom: PD000930; Bac\_OmpA; 1.  
 DR PROSITE: PS01068; OmpA; 1.  
 KW Outer membrane; Porin; Phage recognition.  
 FT NON\_TER 1 244  
 FT NON\_TER 244 244  
 SQ SEQUENCE 244 AA; 26237 MW; C4D18EB27656EDBA CRC64;

Query Match 8.4%; Score 29; DB 2; Length 244;  
 Best Local Similarity 100.0%; Pred. No. 7.9e-21;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 210 TKHFTLKSDVLFNFNFKATLKPEGQALDQ 238  
 DB 119 TKHFTLKSDVLFNFNFKATLKPEGQALDQ 147

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RESULT 7
Q93QR2 ID Q93QR2 PRELIMINARY; PRT; 148 AA.
AC Q93QR2;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Major outer membrane protein (Fragment).
GN OMPA.
OS Erwinia psidii.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Erwinia.
OX NCBI_TaxID=69224;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EP8427;
RA Brown E.W., Davis R.M., Gouk C., van der Zwet T.;
RT "Allelic diversity of the major outer membrane protein (ompA) gene
RT among necrogenic phytopathogenic species: Molecular evolutionary
RT aspects of relatedness.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF220780; AAK68946.1; -.
DR InterPro: IPR001145; Bac_OmpA.
DR InterPro: IPR000498; OmpA_tmcm.
DR Pfam: PF00691; OmpA; 1.
DR Pfam: PF01389; OmpA_membrane; 1.
DR ProDom: PD000930; Bac_OmpA; 1.
FT NON_TER 1
FT NON_TER 148
SQ SEQUENCE 148 AA; 16410 MW; 2BBD1FAC6530167F CRC64;

Query Match
Best Local Similarity 8.1%; Score 28; DB 2; Length 148;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 SDVLFNFNKATLKPEGQALDQLYTOLS 244
DB 111 SDVLFNFNKATLKPEGQALDQLYTOLS 138

RESULT 8
Q93QR1 ID Q93QR1 PRELIMINARY; PRT; 148 AA.
AC Q93QR1;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Major outer membrane protein (Fragment).
GN OMPA.
OS Erwinia psidii.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Erwinia.
OX NCBI_TaxID=69224;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EP49406;
RA Brown E.W., Davis R.M., Gouk C., van der Zwet T.;
RT "Allelic diversity of the major outer membrane protein (ompA) gene
RT among necrogenic phytopathogenic species: Molecular evolutionary
RT aspects of relatedness.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF220781; AAK68947.1; -.
DR InterPro: IPR001145; Bac_OmpA.
DR InterPro: IPR000498; OmpA_tmcm.
DR Pfam: PF00691; OmpA; 1.
DR Pfam: PF01389; OmpA_membrane; 1.
DR ProDom: PD000930; Bac_OmpA; 1.
FT NON_TER 1
FT NON_TER 148
SQ SEQUENCE 148 AA; 16040 MW; 73DDA11D6DFAB00 CRC64;

Query Match
Best Local Similarity 8.1%; Score 28; DB 2; Length 148;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 SDVLFNFNKATLKPEGQALDQLYTOLS 244
DB 111 SDVLFNFNKATLKPEGQALDQLYTOLS 138

RESULT 9
Q93QR0 ID Q93QR0 PRELIMINARY; PRT; 148 AA.
AC Q93QR0;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Major outer membrane protein (Fragment).
GN OMPA.
OS Erwinia psidii.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Erwinia.
OX NCBI_TaxID=69224;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EP3558;
RA Brown E.W., Davis R.M., Gouk C., van der Zwet T.;
RT "Allelic diversity of the major outer membrane protein (ompA) gene
RT among necrogenic phytopathogenic species: Molecular evolutionary
RT aspects of relatedness.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF220782; AAK68948.1; -.
DR InterPro: IPR001145; Bac_OmpA.
DR InterPro: IPR000498; OmpA_tmcm.
DR Pfam: PF00691; OmpA; 1.
DR Pfam: PF01389; OmpA_membrane; 1.
DR ProDom: PD000930; Bac_OmpA; 1.
FT NON_TER 1
FT NON_TER 148
SQ SEQUENCE 148 AA; 16410 MW; 2BBD1FAC6530167F CRC64;

Query Match
Best Local Similarity 8.1%; Score 28; DB 2; Length 148;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 SDVLFNFNKATLKPEGQALDQLYTOLS 244
DB 111 SDVLFNFNKATLKPEGQALDQLYTOLS 138

RESULT 10
Q93QP0 ID Q93QP0 PRELIMINARY; PRT; 148 AA.
AC Q93QP0;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Major outer membrane protein (Fragment).
GN OMPA.
OS Pectobacterium cyripedii.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Pectobacterium.
OX NCBI_TaxID=55209;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=29267;
RA Brown E.W., Davis R.M., Gouk C., van der Zwet T.;
RT "Allelic diversity of the major outer membrane protein (ompA) gene
RT among necrogenic phytopathogenic species: Molecular evolutionary
RT aspects of relatedness.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF220802; AAK68968.1; -.
DR InterPro: IPR001145; Bac_OmpA.
DR InterPro: IPR000498; OmpA_tmcm.
DR Pfam: PF00691; OmpA; 1.
DR Pfam: PF01389; OmpA_membrane; 1.

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Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 SDVLFNFNKATLKPEGQALDQLYTOLS 244
DB 111 SDVLFNFNKATLKPEGQALDQLYTOLS 138

RESULT 9
Q93QR0 ID Q93QR0 PRELIMINARY; PRT; 148 AA.
AC Q93QR0;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Major outer membrane protein (Fragment).
GN OMPA.
OS Erwinia psidii.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Erwinia.
OX NCBI_TaxID=69224;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EP3558;
RA Brown E.W., Davis R.M., Gouk C., van der Zwet T.;
RT "Allelic diversity of the major outer membrane protein (ompA) gene
RT among necrogenic phytopathogenic species: Molecular evolutionary
RT aspects of relatedness.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF220782; AAK68948.1; -.
DR InterPro: IPR001145; Bac_OmpA.
DR InterPro: IPR000498; OmpA_tmcm.
DR Pfam: PF00691; OmpA; 1.
DR Pfam: PF01389; OmpA_membrane; 1.
DR ProDom: PD000930; Bac_OmpA; 1.
FT NON_TER 1
FT NON_TER 148
SQ SEQUENCE 148 AA; 16410 MW; 2BBD1FAC6530167F CRC64;

Query Match
Best Local Similarity 8.1%; Score 28; DB 2; Length 148;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 SDVLFNFNKATLKPEGQALDQLYTOLS 244
DB 111 SDVLFNFNKATLKPEGQALDQLYTOLS 138

RESULT 10
Q93QP0 ID Q93QP0 PRELIMINARY; PRT; 148 AA.
AC Q93QP0;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Major outer membrane protein (Fragment).
GN OMPA.
OS Pectobacterium cyripedii.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Pectobacterium.
OX NCBI_TaxID=55209;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=29267;
RA Brown E.W., Davis R.M., Gouk C., van der Zwet T.;
RT "Allelic diversity of the major outer membrane protein (ompA) gene
RT among necrogenic phytopathogenic species: Molecular evolutionary
RT aspects of relatedness.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF220802; AAK68968.1; -.
DR InterPro: IPR001145; Bac_OmpA.
DR InterPro: IPR000498; OmpA_tmcm.
DR Pfam: PF00691; OmpA; 1.
DR Pfam: PF01389; OmpA_membrane; 1.

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DR ProDom; PD000930; Bac_OmpA; 1.
FT NON_TER 1
FT NON_TER 148
SQ SEQUENCE 148 AA; 16013 MW; 17B9503819ADA12F CRC64;

Query Match
Best Local Similarity 8.1%; Score 28; DB 2; Length 148;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 218 DVLNFNFKATLKPEGQQAALDQLYTQLS 245
DB 112 DVLNFNFKATLKPEGQQAALDQLYTQLS 139

RESULT 11
Q93QR4
ID Q93QR4 PRELIMINARY; PRT; 149 AA.
AC Q93QR4;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Major outer membrane protein (fragment).
GN OMPA.
OS Erwinia psidii.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Erwinia.
OX NCBI_TaxID=69224;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EP8428;
RA Brown E.W., Davis R.M., Gouk C., van der Zwet T.;
RT "Allelic diversity of the major outer membrane protein (ompA) gene
RT among necrogenic phytopathogenic species: Molecular evolutionary
RT aspects of relatedness.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF220778; AAK68944.1; -.
DR InterPro; IPR001145; Bac_OmpA.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA_membrane; 1.
DR ProDom; PD000930; Bac_OmpA; 1.
FT NON_TER 1
FT NON_TER 149
SQ SEQUENCE 149 AA; 16380 MW; 5472FFA455195DD5 CRC64;

Query Match
Best Local Similarity 8.1%; Score 28; DB 2; Length 149;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 SDVLFNFKATLKPEGQQAALDQLYTQLS 244
DB 112 SDVLFNFKATLKPEGQQAALDQLYTQLS 139

RESULT 12
Q93QR3
ID Q93QR3 PRELIMINARY; PRT; 149 AA.
AC Q93QR3;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Major outer membrane protein (fragment).
GN OMPA.
OS Erwinia psidii.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Erwinia.
OX NCBI_TaxID=69224;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EP8428;
RA Brown E.W., Davis R.M., Gouk C., van der Zwet T.;
RT "Allelic diversity of the major outer membrane protein (ompA) gene
RT among necrogenic phytopathogenic species: Molecular evolutionary
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RT aspects of relatedness.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF220779; AAK68945.1; -.
DR InterPro; IPR001145; Bac_OmpA.
DR InterPro; IPR000498; OmpA_tmem.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA_membrane; 1.
DR ProDom; PD000930; Bac_OmpA; 1.
FT NON_TER 1
FT NON_TER 149
SQ SEQUENCE 149 AA; 16346 MW; 4422BFA4550341D5 CRC64;

Query Match
Best Local Similarity 8.1%; Score 28; DB 2; Length 149;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 SDVLFNFKATLKPEGQQAALDQLYTQLS 244
DB 112 SDVLFNFKATLKPEGQQAALDQLYTQLS 139

RESULT 13
Q93QP2
ID Q93QP2 PRELIMINARY; PRT; 149 AA.
AC Q93QP2;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Major outer membrane protein (fragment).
GN OMPA.
OS Erwinia rhapontici.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Erwinia.
OX NCBI_TaxID=55212;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=29283;
RA Brown E.W., Davis R.M., Gouk C., van der Zwet T.;
RT "Allelic diversity of the major outer membrane protein (ompA) gene
RT among necrogenic phytopathogenic species: Molecular evolutionary
RT aspects of relatedness.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF220800; AAK68966.1; -.
DR InterPro; IPR001145; Bac_OmpA.
DR InterPro; IPR000498; OmpA_tmem.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA_membrane; 1.
DR ProDom; PD000930; Bac_OmpA; 1.
FT NON_TER 1
FT NON_TER 149
SQ SEQUENCE 149 AA; 16004 MW; 8E0642C39DFAF216 CRC64;

Query Match
Best Local Similarity 7.6%; Score 26; DB 2; Length 149;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 LFNFNKATLKPEGQQAALDQLYTQLS 245
DB 115 LFNFNKATLKPEGQQAALDQLYTQLS 140

RESULT 14
Q93QO6
ID Q93QO6 PRELIMINARY; PRT; 147 AA.
AC Q93QO6;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Major outer membrane protein (fragment).
GN OMPA.
OS Brenneria rubrifaciens.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Brenneria.
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OX NCBI_TaxID=55213;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BR4790;
RA Brown E.W., Davis R.M., Gouk C., van der Zwet T.;
RT "Allelic diversity of the major outer membrane protein (ompA) gene
RT among necrogenic phytopathogenic species: Molecular evolutionary
RT aspects of relatedness.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF220786; AAK68952.1; -;
DR InterPro; IPR001145; Bac_OmpA.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA_membrane; 1.
FT NON_TER 1
FT NON_TER 147 149
SQ SEQUENCE 147 AA; 16020 MW; 92F431FC41442DC4 CRC64;

Query Match
Best Local Similarity 6.4%; Score 22; DB 2; Length 147;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 213 FTLKSDVLFNFENKATLKPEGOQ 234
Db 106 FTLKSDVLFNFENKATLKPEGOQ 127

RESULT 15
O93QP5
ID O93QP5 PRELIMINARY; PRT; 149 AA.
AC O93QP5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Major outer membrane protein (fragment).
GN OMPA.
OS Erwinia mallotivora.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Erwinia.
OX NCBI_TaxID=69222;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EM8645;
RA Brown E.W., Davis R.M., Gouk C., van der Zwet T.;
RT "Allelic diversity of the major outer membrane protein (ompA) gene
RT among necrogenic phytopathogenic species: Molecular evolutionary
RT aspects of relatedness.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF220797; AAK68963.1; -;
DR InterPro; IPR001145; Bac_OmpA.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA_membrane; 1.
DR ProDom; PD000930; Bac_OmpA; 1.
FT NON_TER 1
FT NON_TER 149 149
SQ SEQUENCE 149 AA; 16100 MW; 3494978343ED9A6C CRC64;

Query Match
Best Local Similarity 6.4%; Score 22; DB 2; Length 149;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 223 FNKATLKPEGGQALDQLYTQLS 244
Db 118 FNKATLKPEGGQALDQLYTQLS 139

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Search completed: April 15, 2003, 08:56:27  
Job time : 71 secs